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                     Meissner R, Lechelt-Kunze C;
                                                                                             22-NOV-2000; 2000DE-1057755
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Matches 2396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 10-12; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding plant phosphomevalonate kinase, useful identifying modulators, potentially useful as herbicides and grow regulators -
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                                                           AATCCGATCTACCACCACTACTCGTACCGCCGGTCATTTACTGCCGCCGATTTCAAATTA
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| 1800 | AAATTAGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTACTGTGCTT | 1741 | Qy |
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| 1740 | AACTGGCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGAGCHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 1681 | Qy |
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| 1680 | CCATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAGGCACGAGAAA | 1621 | Qy |
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| 1500 | TATGTTCGCTTCTCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCA | 1441 | Qy |
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| 1380 1380 | AAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTT | w w | Qy Db |
| 1320 | GTTGCAGCTCTGTTACATTATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAGAAGGA | 1261 | Qу |
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| 1260 | TCCAAGCCTGAAGTAGCAAAAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTG | 1201 | Qy |
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| 1200 | GGTACCCTTGCACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAAT | 1141 | Qy |
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| 1140 1140 | TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG | 0 0 | Qy Db |
| 1080 | GAATCATTGCACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGAC | 1021 | Qy Db |
| 1020 | GTAGAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCAACCGAGAAGGACAAA | 961 | Qy |
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| 960 | CTGTCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTT | 901 | Qy Db |
| 900 | TGGAAATGGACAGATGTCAAATTAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAA | . 841 | Qy |
| | | . 841 | Db |
| 840 | GCACGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCA | 781 | Qy |
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| 780 | ATGACTGGAGGCTACCTTGTACTCGAGAAGCCAAATGCAGGGCTTGTGTTGAGTACAAAT | 721 | Db |

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                                                                                       (GORL/)
(ANYY/)
                                                                                                                                                                   US2002023280-A1
                                                                                                                                                                                                      Arabidopsis thaliana; genetic modification;
                                                                                                                                                                                                                                                                                                                                                                                                                        2221
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                                                                     (HAMI/)
(PRIC/)
                                                                                                                 27-JAN-2000;
                                                                                                                                  26-JAN-2001;
                                                                                                                                                    21-FEB-2002
                                                                                                                                                                                     Arabidopsis
                                                                                                                                                                                                                                 Arabidopsis
                                                                                                                                                                                                                                                                    ABL94086
                                                                                                                                                                                                                                                                                      ABL94086 standard; cDNA; 443
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                                                     (אטאא,
        (WOES/)
                                                              (RAIN/)
                          MATH/)
                                    PAGE/)
                                            RAME/)
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LEDFORD B L. WOESSNER J P. HAAS W D.
                         PAGE A.
MATHEW A V.
                                                      Y DY
                                                                     HAMILTON C M. PRICE J L.
                                                                                               GORLACH J.
                                           RAMEAKA J G.
                                                             RAINES T M.
                                                                                                                                                                                      thaliana
                                                                                                                                                                                                                                thaliana nucleic acid sequence Ref: 2027851 SEQ ID
                                                                                                                 2000US-178502P
                                                                                                                                  2001US-0770444
                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                       gene;
                                                                                                                                                                                                               insecticide;
                                                                                                                                                                                                                                                                                      ΒP
                                                                                                                                                                                                               fungicide;
                                                                                                                                                                                                               plant; mapping;
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Matches 443;

Conservative

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Indels

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Gaps

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1955

384

1896 AATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTCCGATAGAGCCTGAATCTCAAAC

TCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGC AATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTCCGATAGAGCCTGAATCTCAAAC

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TCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGC

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TGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTGAGT TGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTGAGT

84

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263

2135 264 2075

204

TGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCCGGCACCAAACTGACCCA

CCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCACCT

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The present invention describes an Arabidopsis thaliana nucleic acid (I) CC comprising a sequence capable of hybridising under stringent conditions CC to a sequence (S1) selected from any one of the 999 sequences given in CC they can be used as protein expression modulators. (I) can be used in CC identifying homologous or related genes, in producing compositions that CC modulate the expression or function of their encoded proteins, mapping CC functional regions of the proteins, and in studying associated CC physiological pathways. (I) can also be used: (1) for the genetic CC manipulation of cells, particularly plant cells; (2) in screening assays CC of various plant strains to determine the strains that are best capable CC withstanding a particular disease or environmental stress; (3) for CC chancing or inhibiting production of a biosynthetic product in a plant; (4) as probes in mapping and in diagnosis, in genetic modification and CC for screening purposes, to generate additional copies of the nucleic certains to describe a particular disease or any plant cells and as any as a
                                                 Query Match
                               Best
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Garcia CA,
Hurban P;
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(KRIC/)
(SLAT/)
(DAVI/)
(ALLE/)
(HOFF/)
                                                                                                                                                                       acids, to generate ribozymes or antisense oligonucleotides, and as single-stranded DNA probes or as triple-stand forming oligonucleotides; and (5) for generating genetically modified transgenic organisms. Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 851; 44pp; English.
                                                                                                      Sequence
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                       Local Similarity
                                                                                                                                                     web site
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KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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Kricker M,
                                                                                                      BP;
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A, Mathew AV,
                       18.5%;
                                                                                                A; 107
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Score 443; DB 24; | Pred. No. 7.7e-121; 0; Mismatches 0;
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                                                                                                   G; 107
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                                                                                                   T; 0 other;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid (I, ABL60244) that encodes a plant phosphomevalonate kinase (PMVK, ABB77505), excluding the known fully defined partial sequences ABL60245-ABL60247. Plant PMVK, (I), constructs and host cells that contain (I) are used to identify agents that bind to and/or modulate activity of PMVK, potentially useful as herbicides and growth regulators. (I) is also used for recombinant production of PMVK. The present sequence is that of a PMVK encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding identifying modulators, po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2000; 2000DE-1057755
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                                                                                                                                                               GAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCA---ACCGAGAAGGACAAA
                                                                     TCTCGGAAACATTTAACACTTCAGTGTGTATCTTCAAGTGAATCAAGGAACCCTTTTGTA
                                                                                                TCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGTA
                                                                                                                                                                                                                                                             CGTTTTTACGCTATTGTTAAGCCAATTCATGAAGCTATCAAGCCTGAAAGCTGGGCATGG
                                                                                                                                                                                                                                                                                        CGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGG
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the invention.
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 213 A; 151 C; 144
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                                                                                                                                                                                                                                                                                                                                                                                       17.8%;
76.1%;
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and growth
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RESULT 4
ABL60245
PS X F F F F X X F R X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X F R X X E F R X X X E F R X X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X E F R X X
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                                             Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant; metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid; genome mapping; physical mapping; positional cloning; forestry; agriculture; medicine; fermentation; plant development; pest resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCCTCAAACTAAACCTGATTCTTGGGCTTGGGCTTGGTCAGATGTCAGATTAACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACGAAGAAGTCAAAGCCTGAAAGTTGGGCATGGACAGATGGACAGATGTCAAATTAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAATGCTGGACTTGTTACTAGTACTAATGCTCGTTTTATGCTATTGTCAAACCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGACACGGACTCCCTTTGACATCAGAATCATTGGCCACCCTTCCGCCTTTTGCCTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGCCTATGCAACAGCTGACCAGAATAAAAAGGACTTGTTGCACAAACTACTTTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGCTCATTTGGCAAC - - - CGAGAAGGACAAAGAATCATTGCACAAACTCTTATTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAATGCAGGGCTTGTGTGAGTACAAATGCACGGTTTTACGCGATTGTGAAGCCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGGCTCATCTGCAGCAATGACAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAGGTTCTTCTGCAGCAATGACAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAAAAACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTGCATCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTCCTCAAGTGAAACAAGGAACCCTTTTGTGGAATATGCTGTGCAATACTCCGTGGCT
                                                                                                                                                                                           radiata
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                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              (first
                                                                                                                                                                                        phosphomevalonate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                             CDNA; 571
                                                                                                                                                                                                                                              entry)
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71.7%;
                            pine;
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Pred. No. 4.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                           CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523
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TTCAGTCTGT---GTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGT

TGCAAAATGTTGCTTCTTCAAGTAGCAATGGTAATCCTTTTGTGGAACAAGCAGTGCAAT

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                                                                                                                                                                                                                                                                                    The present invention describes plant polynucleotides encoding CC polypeptides involved in the production and modification of isoprenoids, CC such as terpenoid and steroid compounds. The polynucleotides are used CC in genome mapping, in physical mapping and in positional cloning of CC genes. The polynucleotides and polypeptides are useful in forestry and CC agriculture for manipulation of isoprenoid metabolism, in medicine for CC therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms and in fermentation and CC conditions, manipulating isoprenoid pathways or isoprenoid composition CC applications, manipulating isoprenoid pathways or isoprenoid composition CC may, for example, affect plant development, pest resistance, and the CC value of extractives (e.g. pinene and myrcene). The ubiquitous and CC varied roles of isoprenoids make the polynucleotides attractive targets CC analogo and Anbisou to Anbisous in a variety of fields. Analogozo to CC canadata polynucleotides and proteins used in the exemplification of the CC present invention.
                                                                                                                                                                                  Matches
                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New plant polynucleotides encoding polypeptides involved in the production and modification of isoprenoids, useful in forestry agriculture for manipulation of isoprenoid metabolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-431575/37.
P-PSDB; AAB18130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200036081-A2
                                                                                                                                                                                                                                                        Sequence 571 BP; 161 A; 129 C; 136 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 68; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Havukkala IJ
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29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
                                     302
                                                                         743
                                                                                                             242
                                                                                                                            683 AAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTGATGACTGGAGGCTACCTTGTAC
                                                      TCGAGAAGCCAAATGCAGGGCTTGTGTGTGAGTACAAATGCACGGTTTTTACGCGATTGTGA
 AGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAAT
                                                                                                             ACATGGCTGTAGTTGTCAGCTCCTGGTAAGGTTTTAATAACAGGAGCTTATCTAATTC
                                       {	t TTGAGAAGCCAAATCCAGGACTTGTGCTTACCACCAGCTCGCTTCTACGCCATTGTGA}
                                                                                                                                                                                  210;
                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0215504
99US-0146441
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                                                                                                                                                                                                 5.6%;
                                                                                                                                                                                  0;
                                                                                                                                                                                                   Score 135.2;
Pred. No. 2.
                                                                                                                                                                                    Mismatches 103;
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                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                              plant phosphomevalonate kinase (PMVK, ABB77505), excluding the known fully defined partial sequences ABL60245-ABL60247. Plant PMVK, (I), constructs and host cells that contain (I) are used to identify agents that bind to and/or modulate activity of PMVK, plant y useful as herbicides and growth regulators. (I) is also used for recombinant production of PMVK. The present sequence is that of a PMVK encoding DNA excluded by the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE10057755-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth
                                                                                                                                                                                                                     242
                                                                                                                                                                                                                                                                                                             Sequence 571 BP; 161 A; 129 C; 136 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 15; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monterey pine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL60247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL60247 standard; DNA; 571
                                  482
                                                         923
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                                                                                                                                                                                                                               683 AAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTTGATGACCTGGAGGCTACCTTGTAC 742
                                                                                                                                                                                                                                                          Local 210;
                                 TGCAAAATGTTGCTTCTTCAAGTAGCAATGGTAATCCTTTTGTGGAACAAGCAGTGCAAT
                                                                                                                                                                       TCGAGAAGCCAAATGCAGGGCTTGTGTGTGAGTACAAATGCACGGTTTTACGCGATTGTGA
ATGCTATAGCTGCTGC
                                                TTCAGTCTGT----GTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGT
                                                                                                    TAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTGTCACTGAATCATTTGACTC
                                                                                                                          AGCCACTGCGGACTAGCACAGATTCCAGTAGTTGGGCATGGCTATGGACAGATGTGAAAT
                                                                                                                                                AGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAAT
                                                                                                                                                                                                                  ACATGGCTGTAGTTGTGTCAGCTCCTGGTAAGGTTTTAATAACAGGAGCTTATCTAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-445360/48
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                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid encoding plant phosphomevalonate kinase, modulators, potentially useful as herbicides
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lechelt-Kunze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMVK; phosphomevalonate kinase;
                                                                                                                                                                                                                                                                            5,6%;
66,5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                         Score 135.2; DB 2
Pred. No. 2.1e-29;
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                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                      DB 24;
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RESULT 7
AAF22297/c
ID AAF22297;
XX AAF22297;
XX AAF22297;
XX AAF22297;
XX CONTAINAR-200
DT 20-MAR-200
XX CONTAINAR-200
XX CONTAINAR-200
XX CONTAINAR-200
XX CONTAINAR-19
PR 11-MAR-19
PR 11-MAR-19
PR 11-SEP-19
XX (UYCH-) U
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XX PPH PRODUCING
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                                                                                                 RESULT 8
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Best Local
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13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clottin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells
                                                                         AAC37035 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 96583 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 102; Page 716–738; 1449pp; English.
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es 106; Conser
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0; Mismatches
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| 99US-0139453. 99US-0139454. 99US-0139456. 99US-0139456. 99US-0139456. 99US-0139459. 99US-0139460. 99US-0139461. 99US-0139463. 99US-0139463. 99US-0139463. | 99US-0135124 99US-0135353 99US-01356221 99US-0136021 99US-0136782 99US-0137722 99US-01377528 99US-0137752 99US-0137754 99US-0138094 99US-0138847 99US-0139119 99US-0139119 | 99US-0132407 99US-0132485 99US-0132486 99US-0132486 99US-01322863 99US-0134256 99US-0134218 99US-0134219 99US-0134219 99US-0134370 99US-0134364 | 99US-0121825. 99US-0123180. 99US-0125788. 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128714. 99US-0128714. 99US-0130077. 99US-0130077. 99US-0130079. 99US-01300810. 99US-0131449. 99US-0131449. | (first entry) haliana DNA fra assay; genetic ification; sign hway; promoter; haliana. |
| | | | | yment SEQ ID N mapping; gene al transductio termination s |
| | | : | | 15946. xpression pathway; uence; ss |
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| 13 - AUG - 1999; 13 - AUG - 1999; 16 - AUG - 1999; 17 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 23 - AUG - 1999; 23 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 27 - AUG - 1999; | -AUG-1999 | | | |
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RESULT 9
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    Nucleic acid
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nilarity 98.5%;
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99US-0162142
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Pred. No. 7.7e-09;
D; Mismatches 1;
   of prenyl alcohol SEQ ID
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Prenyl alcohol; mutatindustrial synthesis;
WO200253747-A1
                                      Saccharomyces cerevisiae
                                                                                               mutated cell;
                                                                          ed cell; squalene synthase gene; isoprenoid-terpenoid compound; o
                                                                                Вp
                                                                                                   geometric isomer;
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28-DEC-2000; 28-DEC-2000; 18-SEP-2001; ; 2000JP-0401701. ; 2000JP-0403067. ; 2001JP-0282978.

(TOYT) TOYOTA JIDOSHA KK

Obata S;

WPI; 2002-548086/58.

Production of prenyl alcohols by cul mutated cells with reduced squalene transcriptional product culturing translationally-active synthase gene ξ express

Disclosure; Page 237-238; 262pp; Japanese.

The invention relates to a method for producing prenyl alcohol comprising culturing mutated cells, having been mutated so as to reduce the amount of transcriptional product of squalene synthase gene transcriptional activity, and then collecting prenyl alcohol from the culture medium. The method is for the production of prenyl alcohols, which is for use in industrial synthesis of isopremoid-terpenoid compounds particularly physiologically-active prenyl alcohol geometric isomers. This polynucleotide sequence represents a nucleic acid sequence relating to the method for producing prenyl alcohol comprising culturing mutated Sequence 1356 304 G; 389 T; 0 other;

вP; 427 A; 236 C;

Query Match
Best Local Similarity
Matches 138; Conserv Conservative 2.4%; 50.7%; 0; Score 57.6; DB 24; Pred. No. 3.7e-06;); Mismatches 134; Indels Length 0; Gaps 0

ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG 610

GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC 1516

CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC

GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576

ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT 790

TAACTTTATGGATGGGCGATATTAAGAATGGT

ABK96801; ABK96801 standard; DNA; 1356 BP

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                    cc expression recombinant DNA or a DNA for genome integration into a host cwhich contains prenyl diphosphate synthase gene or its variant; and cc (B) collecting product from the culture medium. Also described is: (1) a method for producing prenyl alcohol in which the expression crecombinant DNA contains; (a) a hydroxymethylglutaryl-COA reductase cc gene or its variant; or (b) an isopentenyl diphosphate delta-isomerase cc gene; (2) a process for producing geranylgeraniol, comprising: (c) a constructing a recombinant by transferring an expression crecombinant DNA or a DNA for genome integration into a host which cc contains hydroxymethylglutaryl-COA reductase gene or its variant; and cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc in which the expression recombinant DNA also contains an isopentenyl cc mevalonate delta-isomerase gene, mevalonate kinase gene, or cc mevalonate diphosphate decarboxylase gene. The methods are used for the production of prenyl alcohols, particularly for use in industrial cc synthesis of isoprenoid-terpenoid compounds e.g. physiologically-active crepresent prenyl diphosphate synthase genes and related PCR primers used in the methods of the invention
                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                  1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of prenyl alcohols by culturing a transformant transferred with e.g. prenyl diphosphate synthase gene, for use in industrial synthesis of e.g. physiologically-active isoprenoid-terpenoid compount
                                                                                                                                                                                                                                                                                                                                     Sequence 1356 BP; 427 A; 236 C; 304 G; 389 T; 0 other;
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GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
                                                                                                           GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
                                                                                                                                               GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC 1456
                                                                                                                                                                                    ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                   CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
                                                                        CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
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                                                                                                                                                                                                                                                                                                                                                                              methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on relates to a process for producing a prenyl alcohol (A) construction of a recombinant by transferring an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000JP-0403067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-JP11214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prenyl diphosphate synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muramatsu
                                                                                                                                                                                                                                                                              2.4%; 50.7%;
                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reductase;
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                                                                                                                                                                                                                                                                                Score 57.6;
Pred. No. 3.
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          farnesylgeraniol;
                                                                                                                                                                                                                                                                                  3.7e-06;
                                                                                                                                                                                                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Totsuka
                                                                                                                                                                                                                                                            134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geranylgéraniol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #20.
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ss;
                                                                                                                                                                                                                                                            <u>.</u>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compounds
                                                                                                                                                                                                                                                          Gaps
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RESULT 11
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                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                             Matches
                                                                1397
                                                                                                                                                                                                                                                      (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is yeast phosphomevalonate kinase (PMK; ERG8) EC 2.7.4.2. encoding orf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1577
                                                                                                             1337 ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG 1396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP; isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme; transgenic plant; yeast; phosphomevalonate kinase; ERG8; PMK; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD31013 standard;
 1457 CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
                                                                                                                                                                                                                           Sequence 1356
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the use of specific genes of the mevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 116-117; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-217122/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2000; 2000US-221703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001; 2001WO-US24037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200210398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast phosphomevalonate kinase (ERG8) orf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD31013;
                                                                                                                                                                                                                                                                                                                                                                                                       and isoprenoid biosynthetic pathways and inactive gene sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KUEH/) KUEHNLE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAHN/) HAHN F M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 791
                                 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731
                                                                GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCCTTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŦX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACTTTATGGATGGGCGATATTAAGAATGGT 822
                                 GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
                                                                                                ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT 790
                                                                                                                                                             138;
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      providing transformed cells
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                             427 A; 236 C; 304 G; 389 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                            2.4%; 50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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                                                                                                                                                             0,:
                                                                                                                                                                              Score 57.6;
Pred. No. 3
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                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        having increased isoprenoid
                                                                                                                                                                              3.7e-06;
                                                                                                                                                                                             DB 24;
                                                                                                                                                             134;
                                                                                                                                                                                         Length 1356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1517
                                                                                                                                    kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) synthase (HMGS) and Streptomyces sp. CL190 orf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Operon D DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 77; Page 141-145; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KUEH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2000; 2000US-221703P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAHN
                                                                                                               HMG-COA
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Arabidopsis thal
Streptomyces sp.
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                                                                                                               (HMGRt)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMG-CoA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HMGS; AACT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            730
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Sequence

7681 BP;

2127 Α.

1691

C; 1837

<u>و</u>;

2026 Τ;

0 other;

The invention relates to the use of specific genes of the mevalonate and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance blosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)

Claim 77; Page 127-131;

193pp;

English

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AAD31023
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                       Use of specific genes of mevalonate and isoprenoid biosynthetic pathways, for providing a cell with herbicide or antibiotic resistance, and for providing transformed cells having increased isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1397
                                                                                                                                                                                 Hahn
                                                                                                                                                                                                                                                                                                                                          Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; yeast; phosphomevalonate kinase; HMGRt; mevalonate kinase; mevalonate diphosphate decarboxylase; lacetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1577
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                                                                                              production
                                                                                                                                                         WPI; 2002-217122/27.
                                                                                                                                                                                                                                             31-JUL-2000; 2000US-221703P.
                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                  WO200210398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Operon A DNA encoding mevalonate pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD31023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD31023 standard; DNA;
                                                                                                                                                                                                         (KUEH/)
                                                                                                                                                                                                                                                                   31-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                               MVK; PMK; HMG-CoA reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mevalonate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2002
                                                                                                                                                                                                                     (/HAHN/)
                                                                                                                                                                                                                                                                                                                                                                                                                            isoprenoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765
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                                                                                                                                                                                 ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGTGGGTTTGATGTCAGCTGTGTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAACTTTATGGATGGGCGATATTAAGAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
                                                                                                                                                                                                        KUEHNLE A
                                                                                                                                                                                                                     HAHN F M.
                                                                                                                                                                                Kuehnle AR;
                                                                                                                                                                                                                                                                                                                                           Arabidopsis
                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                             dimethylallyl diphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                          isopentenyl diphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                   2001WO-US24037
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                                                                                                                                                                                                                                                                                                                                             thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57.6;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                          herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   856
                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                       e kinase; HMGRt;
decarboxylase; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                       ance; enzyme;
; HMGS; AACT;
HMG-COA; MDD;
                                                                                                                                                                                                                                                                                                                                                                                           A synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DMAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ARABOUT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 138
                                                                                     Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic plant; yeast; phosphomevalonate kinase; HMGRt; HMGS; AACT; mevalonate kinase; mevalonate diphosphate decarboxylase; HMG-CoA; MDD acetoacety! thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1337
                             WPI;
                                                                                                                                                                                                                                                                                31-JUL-2001;
                                                                                                                                                                                                                                                                                                                                        07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Operon B DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD31024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD31024 standard; DNA; 7695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. Cérevisiae orfs encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) synthase (HMGS) and HMG-CoA reductase (HMGRt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding the entire mevalonate pathway. This operon contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is operon A DNA conditions the products of interest.
                                                                                                                                                                                                                            31-JUL-2000;
                                                                                                                                            (KUEH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoprenoid;
                                                                                                                                                                       (HAHN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                     ŦM,
                             2002-217122/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAACTTTATGGATGGGCGATATTAAGAATGGT 4609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAATCTTTTCCTTGGAGAACCTGGAAGTGGT 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                       HAHN F M.
                                                                                                                                         KUEHNLE A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7693 BP;
                                                                                     Kuehnle AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMG-CoA reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dimethylallyl diphosphate; antibiotic resistance; plant; yeast; phosphomowalocci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                            2000US-221703P
                                                                                                                                                                                                                                                                                   2001WO-US24037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding mevalonate pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2212 A; 1526 C; 1794 G; 2161 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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Pred. No. 9.
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                                                                                                                                                         transgenic plant; yeast; phosphomevalonate kinase; HMGRt; HMGS; Aumevalonate kinase; mevalonate diphosphate decarboxylase; HMG-COA;
                                                                                                                                                                                             Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP; isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
                                                                                                                                                                                                                                                    Operon E DNA
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                                                                                                                                            acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase;
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                                                                                                                           HMG-COA
                                                                                       Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                    encoding mevalonate pathway and IPP isomerase
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                                                                                                                           reductase;
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Best Local Similarity 50.7%;
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increased isoprenoid production compared to non-transformed cells, and for providing a cell with an inserted polynucleotide sequence encoding one or more products of interest. The present sequence is operon E DNA encoding the entire mevalonate pathway. This operon contains a cerevisiae orfs encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK), mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACT) and A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-COA) synthase (HMGS); Streptomyces sp. CL190 orf encoding HMG-COA) reductase (HMGRt) and R. capsulatus DNA encoding IPP
                                                                                                                                                                                                                                                                                                                                                                            1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and isoprenoid biosynthetic pathways and inactive gene sites (pseudogene). Genes of the invention are used to enhance biosynthesis of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP) and isoprenoid pathway derived products in the plastids of transgenic plants and microalgae, for producing herbicide or antibiotic resistant transgenic plants and microalgae, for providing transformed cells with
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(KUEH/) KUEHNLE A R.
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                                                                                   TAACTTTATGGATGGGCGATATTAAGAATGGT
                                                                                                                                                                                                                                                                                        CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG 1516
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                     3, 2003, 18:09:32
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Pred. No. 1e-05;
0; Mismatches 134;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Scoring table: Title: Perfect score: OM nucleic - nucleic search, using sw model Database : Searched: Sequence: Run on: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 May 3, 2003, 16:56:55; Search time 4228 Seconds (without alignments) 16492.508 Million cell updates/sec US-09-988-863A-1 2396 2054640 seqs, 14551402878 residues GenEmbl: * gb_pat: *
gb_ph: *
gb_pl: * gb_ba:* gb_htg:* em_htgo_hum:*
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gb_sts:* em_htg_mam:* em_htg_vrt:* em_htg_other: * em_htg_inv:* em_vi:* em_un:* em_p1:* em_ph: em_ov:* em_or: em_in: gb_sy:* 4109280

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE | RESULT 1 AX441242 LOCUS | 44 | | 4. | 39 | 6 0 ~ | 36 | w w w w | ω ω ω κ | , , , | 20 | æ ~ | 100 | 24 | ωκ | 22 | c 20 | 18 | 16 17 | 15 | 13 | 12 | 10 | | o 7 1 | | ۰. | |) L | Result |
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| yophyta ; core eae; A; | linear PAT | AC004392 AC007213 | AC004482 | AC009992 | AC025781 | AC006136 | AL161503 | AX059543 | AFU//408 AL161498 | AC012561 | AB062089 | AX461275 AC007396 | AB018113 | AB024037 | AC005916 | AC009243 | ABU1/U51 AC019018 | AC023279 | AC023913 | AC009526 | AP002068 | AF262041 | AC005398 | AC004705 | AX441246 | AB011480 | AX441245 | AC079041 | AX441242 | Descript |
| racheophyta; endicots; rabidopsis. | . 02-JUL-2002 | Arabidops Arabidops | Arabidop | - ~ - | | ~ ~ | Arabidops | Sequence Arabidops | Arabidops | Arabidops | Ara | မှ မှ | Ara | Ara | Arabidops | | Arabidops | Genomic s | Arabidops | Arabidops | Are | Arabidops | | | Sec | | Sequenc | | Sequence | ion |

| | 900 | QY 841 TGGAAATGGACAGATGTCAAATTAACATCACCACAGCTCTCGGAGAGAAGCATGTATAAA | |
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| | 840 840 | Qy 781 GCACGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCA | |
| | 780 780 | Qy 721 ATGACTGGAGGCTACCTTGTACTCGAGAAGCCAAATGCAGGGCTTGTGTGTG | |
| | 720 720 | Qy 661 GATTATCTTTGTCACTCTTTGAAAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTG | |
| | 660 | Qy 601 TCCGATCATTTCCGGCGATATCCAATCGCAGACTGAGGTGAATCTGGGGTTTTGATCAGC | |
| | 009 | Qy 541 AATCCGATCTACCACCACTACTGGTACCGCCGGTCATTTACTGCCGCCGATTTCAAATTA | |
| | 540 540 | Qy 481 TTGAGGATCTAAATCGGAAATTGCATTAATACTCATCTCCAATCTCTTCTGAAGAGTCCG | |
| | 480 480 | Qy 421 CGATCCGTCTCGATCGACGGAGAATACGTTTCGATCCGGTTTCGATCCAAATCGGAGAGT | |
| | 420 420 | Qy 361 GAGCGTCGACAGTAAGAGAAGAAGACAGCGATTGTGTGTG | |
| | 360 360 | Qy 301 TTCTCTTTTCATCGGCGACGACGACGTCGAGTTTCTGTCAAAACGTTAACGATCCGACTC | |
| | 300 300 | Qy 241 GTTTCTCGGGTTTCTTCGGAACTCCCAGGCCTAGTTTTGGTTTTATTTTTCACGAGTTTTGC | |
| • | 240 240 | Qy 181 GTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACTGTCGGTTTTTTCGGTTCGG | |
| | 180 180 | QY 121 TCAGAGGTGCCGAACCGAACCGACCCGTAAACCGAAATCCTCAAAAGAATTGCCGÁTCG | |
| | 120 120 | Qy 61 AAGCAAACTGGGGAAGATGAAGATGGAGTGGTGAAGAACAAAACCGTATAACCGTTCGGT | |
| | 60 | QY 1 GTCGACCCACGCGTCCGGGCCGACCTTCTTCTTCCTTAAGACAACACATAATGATAG | |
| 0; | ıps | Query Match 100.0%; Score 2396; DB 6; Length 2396; Best Local Similarity 100.0%; Pred. No. 0; Matches 2396; Conservative 0; Mismatches 0; Indels 0; Ga | |
| | | "Arabidopsis thaliana" taxon:3702" 558 g 677 t | |
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                                                                                                                                                                                                         Town, C.D. and Kaul, S.
Direct Submission
Submitted (17-AUG-2000) The Institute
Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 119420)
                                                                                                   Submitted (19-JAN-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Sep 12, 2000 this sequence version replaced gi:9945156. Address all correspondence to:at@tigr.org
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repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named tindicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AT_rich"
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GSGKTLAFGIPAIMHTKKNKKIGGGSKKVNPTCLVLSPTRELAVQ15DVJLRBAEDF
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GIKSICVYGGSSKGPQ15AIRSGVDIVJGTPGRLRDLLESNVLRLSDVSFVVLLDEADR
MLDMGFEEPVRFILSNTNKVRGMVNFSATWPLDVHKLAQEFMDPIKVIGGSVDLAA
MLDMGFEEPVRFILSNTNKVRGMVNFSATWPLDVHKLAQEFMDPIKVIGGSVDLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(6434. .6529,6641. .6733,6838. .7002,7098. .7191,7285. .7353,7437. .7504,7587. .7643,7723. .7808,7913. .7991,8146. .8226,8316. .8423,8522. .8652,8734. .9220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<6251. .6529,6641. .6733,6838. .7002,7098. .7191,7285. .7353,7437. .7504,7587. .7643,7723. .7913. .7991,8146. .8226,8316. .8423,8522. .8652,8734. /gene="F5M6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4364. .4393)
/rpt_family="AT_rich"
complement(6251. .9220)
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/rpt_family="AT_rich"
complement(3585...3630)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
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                             KLYGAHFKEIAADAPKATKITFDNSDDED"
                                                                                                     NHDYMQI I EVLDERARDQRL I ALLEKY HKSQKNRVLVFALYKYEAERLERFLQQRGWK
AVS I HGNKAQSERTRSLSLFKEGSCPLLVATDVAARGLD I PDVEVVI NYTFPLTTEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to p68 RNA helicase (Schizosaccharomyces
pombe) GI:173419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
complement(3/7)
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complement/2201
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/chromosome="I"
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/cultivar="Columbia"
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                                                                                                                                                                                                                complement(join(<20180 ..20774,20852 ..21024,21105 ..213
21443 ..21617,21696 ..21875,21963 ..22067,22155 ..22292,
22386 ..23390,23481 ..23566,23944 ..24092))</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EINRGEVANGLNCYMKQYGVTKEEASRELRKMYVYRKKVVVEEFMNSHDHVPRQVLLR CLNIARIFDVFYTEGDGYSEPKGKIEHFMTSLYLHPIPLS" complement (14658 . 14692)
                                                                                                                                                       complement(join(20180. .20774,20852. .21024,21105.
21443. .21617,21696. .21875,21963. .22067,22155. .
                                                                                                                                                                                                                                                                                                                                   /translation="MSYFDQDDKEVLAPNSDVIAATTTTATTATHGIEVATEFKPVEH
PVEPLDNDLFIQCFLPEPSILMDGRIMKERVSASMRRKGDLQIVKDEAASESDGSAPK
PPRPPQPNRSILPSILSAPEHNLLLLEECNAMPPVTSKNG"
complement(20180. .24092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDAKEDVRPTGRGGRGVTAKSHVIVTSNMSVRQFLDVKYTTMNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F5M6.6"
toin/1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVLGSLFDVMGEIEREMRPLGRLYRVKQVVEKIKIITKAYQEIAKWARTGHVSTFDEY,
MKVGVLTAGMADYAAYCFIGMEDINEKEAFEWLNSNPLIIKHLTAMFRLANDVGTYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGHDEILLKFAKLNFNFCQFHYVQELKTLTKWWRDLDLASKLPYIRDRLVESHLVALG
PYFEPHYSLGRIIVAKINMIMVVVDDTYDAYATLPQVKALTECLQSIEVSDKLPDYLR
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MDEALSFTRNHLESLTSGNASTASPHLLKHIQNSLYIPRYCNIEVLVAREYISYYEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \mathtt{QQDFFVASSSKKSSDDLESSLPTPHFSPSLWGDHFLSVSLNRAVEFDELEREIETTKP}
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11920. .12138,12229. .12613,12713. .12983,13071. .13334))
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11920. .12138,12229. .12613,12713. .12983,13071. .>13334))
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                                                         /product="G-protein, putative"
/protein_id="AAG50710.1"
                                                                                                                                                                                              /gene="F5M6.7"
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                                                                                                                                                                                                                                                                                                                     /gene="F5M6.7"
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/protein_id="AAG50708.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"terpene synthase family protein, putative"
/protein_id="AAG50729.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical
/protein_id="AAG50726.:
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/gene="F5M6.4"
                                           'db_xref="GI:12321289"
                                                                                                                  gene="F5M6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MEAIRIGFGLPNVHSVPLCLTTTRCLFPRQRLLHSHTPSWKPAK"
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EFSLSDHSPMSESYPENPDALSSPQPKYQLIRVNAKGMNDSCKWVEMFEDVRAVIFCI
SLSDYDQINITPESSGTVQYQNKMIQSKELFESMVKHPCFKDTPFILILNKYDQFEEK
LNRAPLTSCDWFSDFCPVRTNNNVQSLAYQAYFYVAMKFKLLYFSITGQKLFVWQARA
                                                                                                                                                                                                                                                                       RFMCALFSLPVPQGQPRGTVQPSSNYATVPNYIEHKKIQKLLLLGIEGSGTSTIFKQA
KFLYGNKFSVEELQDIKLMVQSNMYRYLSILLDGRERFEEEALSHTRGLNAVEGDSGG
EEANDEGTVTTPQSVVTLNPRLKHFSDMLLDIIATGDLDAFFPAATREYAPLVEEVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEMADLLNCLLPPQKLKPGRYWYDKESGLWGKEGEKPDRVISSNLNFTGKLSPDASNG
NTEVYINGREITKLELRILKLANVQCPRDTHFWVYDDGRYEEEGQNNIRGNIWEKAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASVSPVSGHRQNGNQVRRPVVKFKPVDDHDRIEGREAAEEEDNNVEAETERERKVHE
CTASTKRRKKKKSECYRCGKAKWENKETCIVCDEKYCGNCVLRAMGSMPEGRKCVSC
IGQAIDESKRSKLGKHSRVLSRLLSPLEVKQIMKAEKECTANQLRPEQLIVNGYPLKP
RDRANVDEGFKYVREVLKWDEEKEESYLNGGGEDSFYSTDMSSSPYRPEE"
                                                                                                                                                                                                                              DPA I QATYRK DELHFL PDVAEYFL SRAMEVSSNEYEPSERD I VYAEGVT QGNGLAFM
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complement(24371. .24395)
/rpt_family="AT_rich"
25457. .27277 /note="contains multiple PPR domains: PF01535: PPR repeat"
<25457. .>27277 /gene="F5M6.8"

Query Match Best Local Similarity Conservative 31.7%; 0; Score 759; DB 8; Pred. No. 1.4e-192; Mismatches 0; Length 119420; Indels 484; Gaps 4.

1100 AGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTTGCACCGTTTG AAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTGGTTGCAGCTCTGTTACATT 1279 CATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAA 1219 AGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCCTTGCACCGTTTG 29019 ATCTTGGAGTGGCTGACCTATCTGATCCATGTAAAGAAGGAAAGTTTGGCTGTTCTGATC 1339 CATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAA 1159 28959

TAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCGGAA 1399 ATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAGAAGGAAAGTTTGGCTGTTCTGATC 28839

GTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTCCAG 1459 28779

GTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCCAG 28719

AAGTCTTGTCATTTGCTCAGGTTCATAACGAGAAGTTTGTTGTATATAAATTCTCCACTA 28659 AAGTCTTGTCATTTGCTC-----1477

AGGAAGGGAATTTTACTGACTCCCAAGTTTTGTAGGTTGCAGTAACAGGTCTGCCATTAA AGGTTGCAGTAACAGGTCTGCCATTAA 1504 28599

ATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTT ATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTT 1564 28539

TACCACCACTGATGAATCTT-----1584

28418 AAGATGTTGTCTTATTTAGTTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCACACCATC CTGTTGTGAACTTCACCAACTTCTTATTTCTTTGACTTCTGTGAAATCTGGTGTACTAAC TACCACCACTGATGAATCTTGTAAGCAAACAATCAGACCTAAATTCTTACCTAGAAAAAAC 28479 TTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCACACCATC 1625 28359 28419

| Qy 1432 A | | | RESULT 4 |
|----------------------------------|---|--|---------------------|
| 601 | : | | 2733 |
| 1372 | | AAATAAAGTTGATTTCAAATCTTCTCA 2382 | Qy 2356 |
| Qy 1316 - Db 541 C | | IGIAAGCATTTTATACCCATTGTAAGGTCTTTAACTCTTGGAAAACTTGCGGGAAAATA 2355 | рь 27398 |
| | | OTIVITITICULAR CONTRACTOR CONTRAC | . د |
| _ | | GTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACTTTGGGTGCTAAATTTCTTGG 22 | Qy 2236 |
| Db 421 T | | | Db 27518 |
| Qy 1201 T | | GGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGC 22 | 21 |
| Db 361 G | | 8 GAAGATCCACATGGCGTTTGCCTAGAAAGTGGTGATCCACGAACCACGATGTATTACTTCA 27519 | Db 2757 |
| Qy 1141 G | | | Qy 2116 |
| | | | 2763 |
| Oy 1081 T | | | Оу 2056 |
| Qy 1021 G | | 6 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGAT 2055 | Qy 199 Db 2769 |
| Db 181 G | | 8 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 27699 | Ģ |
| Qy 964 G | - | 6 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995 | Qу 193 |
| рь 121 т | | TCCGCATTTAGAACAAATTGACTTCATCATAATTGACCTCGAGGGACCATGGAATTGCAG 27759 | Db 27818 |
| Оу 904 Т | | 5 | Оу 193 |
| Db 61 T | • | 3 AATAATACTCGTCTGGCTGTAGAATCTTAACAGCATACATGATATACGGGTTCCACAAAT 27819 | Db 27878 |
| ОУ 844 А | | 5 1934 | Qy 1935 |
| pb 1 c | | TIGATAGTIGCTICAGAICTCAACGGACCATTIGIGCAIGATTACTIAGIGCTGIIGCAI 27879 | Db 27938 |
| Qy 784 C | | 5 1934 | Qy 1935 |
| Best Loca Matches | | | Db 27998 |
| Query Mat | • | | Qy 1896 |
| BASE COUNT ORIGIN | | S AATCAACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAAGCTATGTTGAGGATCAG 1895 | Qy 1836 Db 28058 |
| FEATURES | | CAGTTTGGTTCATTTGACTTTTGTATCTCATGTTTAGTGGGTGTTACATGCTACTGAACC 28059 | Db 28118 |
| JOURNAL | | | Оу 1811 |
| REFERENCE AUTHORS TITLE | | 5 TGAAA | Qy 1806 Db 28178 |
| | | AGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTAGTGTGTGCTTACTTC 28179 | Db 28238 |
| ORGANISM | | | Qy 1746 |
| ACCESSION VERSION KEYWORDS | | S GCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGAGCAAATT 1745 | Qy 1686 Db 28298 |
| AX441245 LOCUS DEFINITION | · | | Db 28358 |

| 432 AGTCAGCGTTATGTTCGCTTCTCTCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAAC | 0у 1 |
|--|---|
| 372 CATTGTCTTGCACAAGGGAAGGTCGGAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGA | Qy 13 |
| 316AAGGAAAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTC | Qy 1: |
| 261 GTIGCAGCICTGTTACATTATCTIGGAGIGGTIGACCTATCTGAICCAIGTAAAG | Qy 1; |
| 201 TCCAAGCCTGAAGTAGCAAAAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTG | Qy 1: |
| 141 GGTACCCTTGCACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAAT | Qy 1: |
| 081 TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG | Qy 10 |
| .021 GAATCATTGCACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGAC | Qy 10 |
| 964 GAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCAACCGAGAAGGACAAA | Qy S |
| 904 TCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGTA | Qy S |
| 844 AAATGGACAGATGTCAAATTAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAACTG | Db s |
| 784 CGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCATGG | ФФ |
| ry Match 17.8%; Score 425.4; DB 6; Length 728; tLocal Similarity 76.1%; Pred. No. 6.3e-103; ches 554; Conservative 0; Mismatches 162; Indels 12; | Query Best Match |
| Т 213-а | BASE CO |
| 0 | AUTH TITI JOUR ATUR |
| upland cotton. NISM Gossypium hirsutum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot Rosidae; eurosids II; Malvales; Malvaceae; Gossypium. | SOURCE ORGANIS |
| 945 AX441245 728 bp DNA linear PATTION Sequence 4 from Patent EP1209236. 9100 AX441245 1 GI:21690241 | AX441245 LOCUS DEFINITI ACCESSION VERSION |

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RESULT 5
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                                                                                                                                                                                                                                GGTCTTGATATAACAATATTAGGCTCCAATGACTTTTACTCATATCGGAACCAGATAGAA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCCTCAAACTAAACCTGATTCTTGGGCTTGGGCTTGGTCAGATGTCAGATTAACATCT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGAAGAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGATGTCAAATTAACATCA 870
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    TTAGGTTCTTCTGCAGCAATGACAACAG
                                                                  ACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAAAAACTGGC 1227
                                                                                                                             AGACACGGACTCCCTTTGACATCAGAATCATTGGCCACCCTTCCGCCTTTTGCCTCCATT 523
                                                                                                                                                                     TCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTGCATCAATC 116
                                                                                                                                                                                                            GGTCTTGACATTACAATTTTGGGTTCCAATGATTTTTATTCTTATAGGAATGAGATTGAG
                                                                                                                                                                                                                                                                                                  GCCGCCTATGCAACAGCTGACCAGAATAAAAAGGACTTGTTGCACAAACTACTTTTGCAA 403
                                                                                                                                                                                                                                                                                                                                          GCTGCTCATTTGGCAAC---CGAGAAGGACAAAGAATCATTGCACAAACTCTTATTGCAA 1047
                                                                                                                                                                                                                                                                                                                                                                                    GTTTCCTCAAGTGAAACAAGGAACCCTTTTGTGGAATATGCTGTGCAATACTCCGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGTATGCTATAGCT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCAACTCTCCAGAGAAGCCTTCTATAAATTAGCACTCAAAAATCTTACCATCCAAACT 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAATGCAGGGCTTGTGTTGAGTACAAATGCACGGTTTTACGCGATTGTGAAGCCAATC 810
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                                            TCTTTCAATACTGATGCTAATGGAAGGAATTGTAAGCCTGAAATTGCCAAAACTGGT 583
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c~MPI7
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://ccR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/wetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRAAscan SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scructural analysis of Arabidopsis, thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned PI and TAC clones DNA Res. 5 (2), 131-145 (1998) 98344145
                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MVA3 and the 3' clone is MCM23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        АВU11480 BA000015
AB011480.1 GI:29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (strain:Columbia) DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 40548)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids II; Brassicales;
/translation="MASLFSSRLGSQSLSLLINIFFIFLIFLHEASQTPPPSGSIQTL NSFAGGDSDSCSGGLASLDDHASKCSYIRSQSKCGPQGYITYLKIFFCIFFQSPVLGH LLYLSAWLFYLFYLLGDTAASYFCPSLDSLSKYLKLSPTMAGVTLLSLGNGAPDLFSVV VSFTRSNNGDFGLNSILGGAFFVSSFVVGTICYLIGSRDVAIDRNSFIRDVYFLLVAL CCLGLIIFIGKVTIWVALCYLSIYLLYVGFLSVSHFFDRKKRMSDQILRSREDLAEMG
                                                                                                                                                                                           /note="contains similarity
gb|AAD25785.1
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complement(3187. .4899
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                                                                                                                                                                                                                                                                                                                                                                                                          1. .40548
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:2924730
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                                                                                                                                                                                                                                                           . 4899)
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                                                                                                                                                                                                                                                                                                                                                                                    thaliana"
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                                                                                                                                                                                                                                  to unknown protein
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me 5, Pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Louis,
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CYRFSSQVIAEFVEKGLVASLARAKQEELIKAPEVIICIPMDTRQRSSFRLQAGRNAM
                                                                                                                                                                                                                                                     EYDELEGSGETKAMPKSGLVAEHIESIFLDTSNVKFDVKHDAFKNMFNLKFLKIYNSC
SKYISGLNFPKGLDSLPYELRLLHWENYPLQSLPQDFDFGHLVKLSMPYSQLHKLGTR
                                                                                                                                                                                                                                                                                                                                                                                                                               HRDKLYDKRILVVLDDVRDSLAAESFLKRLDWFGSGSLIIITSVDKQVFAFCQINQIY
TVQGLNVHEALQLFSQSVFGINEPEQNDRKLSMKVIDYVNGNPLALSIYGRELMGKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKALEELILSGCSKLNEFPETWGNMSRLEILLLDETAIKDMPKILSVRRLCLNKNEKI
SRLPDLLNKFSQLQWLHLKYCKNLTHVPQLPPNLQYLNVHGCSSLKTVAKPLVCSIPM
KHVNSSFIFTNCNELEQAAKEEIVVYAERKCHLLASALKRCDESCVPEILFCTSFPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WLKFPLKEVPQDFNPGNLVDLKLPYSEIERVWEDNKDAPKLKWVNLNHSKKLNTLAGL
GKAQNLQELNLEGCTALKEMHVDMENMKFLVFLNLRGCTSLKSLPEIQLISLKTLILS
GCSKFKTFQVISDKLEALYLDGTAIKELPCDIGRLQRLVMLNMKGCKKLKRLPDSLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNFPKLSKDFVHYTKGNPLALQMLGKELLGKDESHWGLKLNALDQHHNSPPGQSICKM
LQRVWEGSYKALSQKEKDALLDIACFRSQDENYVASLLDSDGPSNILEDLVNKFMINI
YAGKVDMHDTLYMLSKELGREATATDRKGRHRLWHHHTIIAVLDKNKGGSNIRSIFLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(9595...10290,10376...11266,11359...11673,
11914...13096,13164...13645))
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VCEEKWSK PCAVVSTALAPVLLTELYCSHYSGSQRNLILY ISGSIGLIVGILAVLTT
EKSHPPKKFSLVWLLGGFTKSVTWTVMIAQELVSLLTSLGYIEGISPSVLGLTVLAWG
NSLGDLIANVTVAFHGGNDGAQIALSGCYAGPLFNTVIGLGVPLVISSLAEYPGVYII
<u>TDLVPWMQKPISGFSMSVVVSFQDDYHNDVGLRIRCVGTWKTWNNQPDRIVERFFQCW</u>
                                                                                    KIMGFPRNLKKLYVGGTAIRELPQLPNSLEFLNAHGCKHLKSINLDFEQLPRHFIFSN
                                                                                                                                                                         SGCTEIKCFSGVPPNIEELHLQGTRIREIPIFNATHPPKVKLDRKKLWNLLENFSDVE
                                                                                                                                                                                                                      VKDLVMLKRLILSHSLQLVECDILIYAQNIELIDLQGCTGLQRFPDTSQLQNLRVVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIDLECVINLATVISNNHVMGKLVCLNMKYCSNLRGLPDMVSLESLKVLYLSGCSELE
                                                                                                                                                                                                                                                                                                                                              HYFPRLAIDVLVDKCVLTISENTVQMNNLIQDTCQEIFNGEIETCTRMWEPSRIRYLL
                                                                                                                                                                                                                                                                                                                                                                                           EMETAFFELKHCPPLKIQDVLKNAYSALSDNEKNIVLDIAFFFKGETVNYVMQLLEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKAVFNHMSTDYDASCFIENFDEAFHKEGLHRLLKERIGKILKDEFDIESSYIMRPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="disease resistance protein-like"
/protein_id="BAB11222.1"
/db_xref="GI:10177890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMPSWFSHDAIGSMVEFELPPHWNHNRLSGIALCVVVSFKNCKSHANLIVKFSCEQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIKKGSKILITTSDKSLMIQSLVNDTYEVPPLSDKDAIKHFIRYAFDGNEGAAPGPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLATKFLQGLLKVENANIESVQAAHEAYKDQLLETKVLVILDNVSNKDQVDALLGERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKLRFGSDETTRT IGVVGMPG IGKTTLATMLY EKWNDRFLRHVL I RDI HEASEEDGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVSSDEDEVINIIIRKVKEILNRRSEGPPSKCSALPPQRHQKRHETFWGIELRIKQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVIPIFYKVQPVTVKELKGDFGDKFRELVKSTDKKTKKEWKEALQYVPFLTGIVLDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="disease resistance protein"
/protein_id="BAB11221.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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/db_xref="GI:10177888"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSELVEEIVRDVYGKLYPAERVGIYARLLEIEKLLYKQHRDIRSIGIWGMPGIGKTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGHVVVPVFYGVDSLTRVYGWANSWLEAEKLTSHQSKFVYIILFSFVKNKILSNNVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSDITRKWCFYRHAFAMMRDLRYLKIYSTHCPQECESDIKLNFPEGLLLPLNEVRYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTSSSSWVKTDGETPQDQVFINFRGVELRKNFVSHLEKGLKRKG
INAFIDTDEEMGQELSVLLERIEGSRIALAIFSPRYTESKWCLKELAKMKERTEQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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2KKSTAHHRKTRPKKTQPWDIKRKPTVYAPLPPLPAEWSPFTLASDDGGAATAAGDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISVFVDACGLQETKFFSIKQNQPLTDGARVLVVVISDEVEFYDPWFPKFLKVIQGWQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MEPPAARVTPSIKADCSHSVNIICEETVLHSLVSHLSAALRREG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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CDS

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Matches Best Query Match

233;

Conservative

0;

Local

Similarity

9.5%; 95.9%;

Score 227; DD ;, Pred. No. 1.1e-49;

Length 40548;

0

Gaps

0

24896

78 TGAAGATGGAGTGGTGAAGAACAAAACCGTATAACCGTTCGGTTCAGAGGTGCCGAACCG 137

TGAAGATGGAGTGGTGAAGAACAAAACCGAATAACCGTTCGGTTCAGAGGTGCCGAACCG 25015

18 GGCCGACCTTCTTCTTCCTTAAGACAACACATAATGATAGAAGCAAACTGGGGAAGA 77

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EQEPVHSLVHDAEEETHNDQTMDIEVDSVNASAQNVGSEETSPSESDRELTWSDKSVV
                                        GPEEIHSTSNETETRTSEVGENSMHVTGEASLVMREHSTPLEESPDVVHDIAETSVNK
SVVEEIMYEEEEAQKQKDEVSPQTFNADIPIDSYASLSSGAVEYVETHSFNDEDVAQL
                                                                                                                                                                                            LERLANEGTSYYPFERQLSEVSESKYSSIPDTESYCTYLEDDEKKVDENNADRETKIA
KYDMYSDNDEENNHSASDHDEENSHSASDHDEEKSHSSEDSDFDEQADSKKLHHDVAE
IVLGSGETHHEQSDMMEGETSDKGKLDEVSDSDSSLSEKEEKIRDISEDEAMLISEQV
                                                                                                                                                                                                                                                                                                                                                                                        QMDVSPVSPWRPMRHEEDEDDDADRDDSLDSGSDGAESSSPDASMTDIIPMLDELHPL
LLSEAPTRGIVDGEGSDAASEGPHRSSSDEGMESDGDSESHGEEGDNENEDEEEDEEE
EDEEEKQEKKEDKDDESKSAIKWTEADQRNVMDLGSLELERNQRLENLIARRRARHNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTDWSNPWTSNDPLREKYNKKMAGMDAPIAKPKGSKKMKDWES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLETKQIVVEEVRKDEEIRKNILLEEANIGDVETDDELNEAEEYEVWKTREIGRIKRE
RDAREAMLREREEIEKLRNMTEQERRDWERKNPKPLSAQPKKKWNFMQKYYHKGAFFQ
ADPDDEAGSAGTDGIFQRDFSAPTGEDRLDKSILPKVMQVKHFGRSGRTKWTHLVNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSVTAGVSESAIAVREKLKGGIGQTKVRRYWPGKAPEWAEEAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene_id:MPI7.7"
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IVTSVSQGVRRMLNKGILDTVTESQGVVVRKCEVTAILILYGLPRLLTYGYILAHEMMHA
YLRLNGYRNLNMVLEEGLCQVLGYMWLECQTYVFDTATIASSSSSSRTPLSTTTSKKV
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join(22096. .22104,22214. .22294,22391. .22507,22593
22878. .22949,23030. .23148,23223. .23281,23363. .237
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EDTRELQIALIESKKIKKIKQADERDQIKHADEREQRKHSKDHEEEEIESNEKEERRH
                                                                                                                  VDLHEELGASSLPSFGELEINMARGVEDDYHHDEARAEESFITAHPSLDESAIHVLCG
LGDGDHEEPVYDSSPPSGSRFPSFSSVSSDYKPDLPEKNGEFIEENEEKEREVYSESI
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DLPYEPNEEKPDLKGDGFQEEFSSQQPKDPMFRRHESFSVGPSMLGGPRHDRLRPFFV
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/db_xref="GI:10177893"
/translation="MISDRSEFRVQIRRLFMIMIRTSYKWICNHPFLLGFVAFLYYLH
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/protein_id="BAB11224.1"
/db_xref="GI:10177892"
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/protein_id="BAB1123.1"
/db_xref="gi:10177891"
/translation="MNEISDLRGMYHKPCYKELRHPNCYVCEKKIPRTAEGLKYHEHP
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/note="emb|CAB16816.1|
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                                                                                                                                               ATGCTATAGCTGCTGC 995
                                                                                                                                                                                  TTCAGTCTGT---GTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATACAGT 979
                                                                                                                                                                                                                       TAACATCGCCTCAGCTTGCAAAGGAGGCCATCTACAAGCTATCTCTGAAGACTCTTAGCC
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                                                                                                                        TTGCTGTTGCAGCTGC
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Sequence 273
AX461344
AX461344.1
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Pinus radiata
Eukaryota; Viridiplantae; Streptophyta; Emb
Spermatophyta; Coniferopsida; Coniferales;
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Sequence 5
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  cress
                                                 273 from
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/db_xref="taxon:3347"
129 c 136 g 145
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from Patent EP1209236
                           GI:21726552
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Pred. No. 5.7e-
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Pinus; Pinus.
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AC004705
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
             Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtownetigr.or. On Apr 18, 2002 this sequence version replaced g1:6598440.
                                                                                  Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 89840)
                                                                                                                                                                      1 (bases 1 to 89840), Rounsley, S.D., Kaul, S., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adam Somerville, C.R. and Venter, J.C.
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Arabidopsis
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                                                              Direct Submission
                                                                     Town, C.D. and Kaul, S.
                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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71.2%;
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chromosome
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DNA line 2 clone F26C24

C24 map mi398,

PLN 11-MAR-2002 ni398, complete

Research,

9712

Adams, M:D.,

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271 TAGTTTTGGTTTTATTTTTCACGAGTTTTTGCTTCTCTTTTCATCGGCGACGACGACGTCGA
                     TTGCATTAATACTCATCTCCAATCTCTTCTGAAG
                                                                             CGATAGTGTGTCGATTCGTCATTGATCCAAATCGGAGAGTTTAAGGTTCGAAATCGGAGA
                                                                                                  AGAATACGTTTCGATCCGGTTTCGATCCAAATCGGAGAGTTTGAGGATCTAAATCGGAAA
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ATTTATTGATACTCATCTCCAATCTCTTCTGAAG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Arah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
341 c 264 g 648 t
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 123.2;
Pred. No. 9.3e
0; Mismatches
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240
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complement(8119. 8212)
/rpt_family="AT_rich"
complement(8308. 8384)
/rpt_family="(TA)n"
8429. 8488
'rpt_family="(TA)n"
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/rpt_family="AT_rich"
complement(2591..2623)
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/note="overlap with BAC clone T26I20 (AC005396:1. .8743)."
complement(977. .1852)
/gene="At2g14850"
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complement(977. .>1852)
/gene="At.2914850"
complement(977. .1852)
                                                             complement(9506. .9541)
/rpt_family="AT_rich"
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/rpt_family="AT_rich"
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KSEFDKLCSKTVGRENISLHNRLVRSILKNASVAKSPPPRYPKKSLYGDPVFPPSPRK
CRSRKFRDRPSPLGPLGKPQSLTTTNDESMSKAQRLPMEVVSVEDGEEVEQMTGSPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAM14999.1"
/db_xref="GI:20197261"
                                                                                           comprement(9363. .9416)
/rpt_family="(TAAAAA)n"
complement/orcol
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/rpt_family="AT_rich"
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complement/2701
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/codon star
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="2"
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13033. .13073
/rpt_family="AT_rich"
13112. .13139
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complement(13155. .13207)
/rpt_family="AT_rich"
13437. .13464
/rpt_family="AT_rich"
complement(24067. .24123)
                                                                                                                                            CSTP I WPPMMYKDAGSRLHALLREVI TQTGLEKNLLGNHPVSRSTESRSPPPAFASDA
LINISSSSHTQEGNNLPDGYSVAGNGEYSKSAVSE I VE I DVPASAGSYMKSSSPGLAA
AAARKGVPAVDRQNSET LYYADDEDGNRKKY SRRGPLRHK FLRALLPFWSSALPTLPV
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18462...18716,18946...19017,1
20623...20703,20991...21014))
/gene="At2g14835"
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18462 ...18716,18946 ...19017,19802 ...19896,19995 ...20112,
20623 ...20703,20991 ...21077,21278 ...21340))
/gene="At2g14835"</pre>
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/gene="At2g14835"
/note="F26C24.16; support
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complement(15170..16350)
/gene="At2g14840"
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complement(14367..1439
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complement(13587. .13750)
/rpt_family="AT_rich"
complement(14259. .14289)
                                                                                                                                                                                                                                                                                                                                      complement(join(22434. .23006,23094. .23225,23400. .23874,
25464. .25603,25684. .25728))
/gene="At2g14830"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="F26C24.3; predicted by genscan"
complement(join(<22434. .23006,23094. .23225,23400. .23874,
25464. .25603,25684. .>25728))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(22434. .25728)
/gene="At2g14830"
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/db_xref="GI:20197262"
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/translation="MYVCKCKKATRLYCFVHKAPVCGECICFPEHTAPAGYYCPA
DGEYDQPKCCQCQATFDEGAGHQVTRLGCLHAIHTSCLVSLIKSFPPHTAPAGYYCPA
                                                                                                         QSVFRFRESTEDERKERKRLRRKPRSTSSSSSPIAKDVDCWRYYYKGKRSRQRKECGK
                                             23985.
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0. .14755
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                                                                                                                                                                                         Arabidopsis thaliana.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 92524)
Direct Submission Submitted (09-MAR-2000) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 AC005398 92524 bp DNA linear PLN 11-MAR-2002 Arabidopsis thaliana chromosome 2 clone T6B13 map mi398, complete
                                                                                                                                          Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M., Shea, M., Ronning, C.M., Fraser, C.M., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                             HTG
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TRCAABYLGMHETVEKONLIYKIDVFLSSSLERSWKDSIIVLGYTKAFFLPLSBDLKLV
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DYYKRVIMNIKYKCILGGEVIGEALKAYGYRRLSGFNKGVMEQGDLVKHXTIIETLVW
LLPAEKNSVSCGFLLKLLKAVTMVNSGEVVKEQLVRRIGQQLEEASMAELLIKSHQGS
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SKIRSLIMSKKIFGKKVQLQSKGGGEKNNGGGGGGSDSSESLGSMNAAEETAKTATPS
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DSYLTEIAKDPNLPASKFIDVAESVTSIPRPAHDALYRAIDMFLKEHPGITKGEKKRM
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/db.xref="G1:3252807"
/translation="MKFMKIGSKLDSFKTDGNNVRYVENELASDISVDVEGSRFCLHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(26952.
29327. .29388))
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complement(join(<26952. .27545,27629...28807,29006.
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/gene="At2g14820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="At2g14820"
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                                                                                                                                                                                                                                                                                                                                                               GI:20197379
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71.28;
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Pred. No. 8.6e-22;
0; Mismatches 68
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.c
On Apr 18, 2002 this sequence version replaced gi:6598467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-FEB-2002) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(2577...2675,2804...2913,3018...3146,3235...3301.3382...3464,3835...3916,3981...4057,4402.4559...4628,4729...4817,4895...5587,5682...5985))
/gene="Att2g14740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding EGF like domain signature" (2014) 2013, 3018. 3146, complement (3016) 2291. 2675, 2804. 2913, 3018. 3146, 3235. 33018. 3823. 3464, 3835. 3916, 3981. 4057, 4402. 4485, 4559. 4628, 4729. 4817, 4895. 5587, 5682. >5985))
//gene__Mat2g14740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="overlap with BAC clone (AC004705:73373. .89840)." complement(1899. .2091) /rpt_family="AT_rich".
                                              /translation="MDPYVAKYYWSMKFFDKHAVDKYLRIGENTLMSCMIHSVEAIIY
LFGKEYLRRPTRQDLKRLLRIGELRGFLGMTGSIDCDKDSLFATNQEVCRKDVERAFG
VLQARFAIVTNPTLI"
                                                                                                                                                                                                                                                              /note="T6B13.5; predicted by genscan" complement(join(<7571..7686,8006..8)/gene="At2g14730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEKLKKAISGGDMVNLNLDWREAVPHPDDRVEYELWINSNDECGVKCDMLMEFVKDFK
GAAQILEKGGFTQFRPHYITWYCPHAFTLSRQCKSQCINKGRYCAPDPEQDFSSGYDG
KDVVVENLRQLCVYKVANETGKPWVWWDYVTDFQIRCPMKEKKYNKECADSVIKSLGI
                                                                                                                                                                                                               complement(join(7571. .7686,8006. .8191,9280./gene="At2g14730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
complement(6732. .6761)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLKALCSGFEETTEPAICLSTDVESNECLDNNGGCWQDKSANITACKDTFRGRVCECP
TVDGVQFKGDGYSHCEPSGPGRCTINNGGCWHEERDGHAFSACVDKDSVKCECPPGFK
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CFFALKVWNAQKAGASAVLVADNVDEPLITMDTPEEDVSSAKYIENITIPSALVTKGF
                                                                                                                                                                                                                                                                                                             /gene="At2g14730"
/note="mfp1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6613. .6657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSAWAAVWLIMLSLGLAAAGAYLVYKYRLRQYMDSEIRAIMAQYMPLDSQPEIPNHVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative vacuolar sorting receptor"
/protein_id="AAM15053.1"
/db_xref="GI:20197383"
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/note="TKP17
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                                                                                                                                               /product="hypothetical protein"
/protein_id="AAM15054.1"
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    rpt_family="AT_rich"
                                                                                                                         /db_xref="GI:20197384"
                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="T6B13.4; identical to GB:U79960; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="T6B13"
                                                                                                                                                                                                                                                                                                                                                                                                                            _family="AT_rich"
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/rpt_family="AT_rich"
complement(17585...17630)
/rpt_family="AT_rich"
complement(17680...17700)
/rpt_family="AT_rich"
complement(17826...17846)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<14856. .>15944)
/gene="At2g14710"
complement/146"
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16650. .16767
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/gene="At2g14710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPLHCTFVPSLVPVPAPCRREEQAELQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPNLPDLVETVKFSNPSYFIEGKRLVVCSRDNTGHAWIYILGDSKLISKTRIECVVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mahlknlpwelleeilsrvppkslvrfrtvskQwnalfddktfi
NNHKMTFRFILATKSKIYSVSIDPVIVVRELPLGIPGLESLELNNLVDCNELLVCVKN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(14856. .15944)
/gene="At2g14710"
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KSAWAAVWLIMLSLGLAAAGAYLVYKYRLRQYMDSEIRAIMAQYMPLDSQPEVPNHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSRKIDKCMGDPDADLDNPVLKEEQDAQVGKGTRGDVTILPTLVVNNRQYRGKLEKSA
VLKALCSGFEESTEPAICLSTDMETNECLDNNGGCWQDKSANITACKDTFRGKVCVCP
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                                                                                                                                                                                                                                                                                                                complement(17155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGAVVWNPWLGQSRWIQPSLNHSPMVFDGIVYDNKKYKMVAFSGLWKIYDFSSDVWID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
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/db_xref="GI:20197380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVDGVRFKGDGYSHCEPSGPGRCTINNGGCWHEERDGHAFSACVDKDSVKCECPPGFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKQLLCYLPWLLLLSLVVSPFNEARFVVEKNSLSVTSPESIKGT
HDSAIGNFGIPQYGGSMAGTVVYPKENQKSCKEFSDFSISFKSQPGALPTFLLVDRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative vacuolar sorting receptor"
/protein_id="AAM15052.1"
/db_xref="GI:20197382"
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                                                                                                                                                                                                                                                                                                                                          bt_family="Rf:ATR0062|AF013294 T18A10 repeat 1
10416"
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                                                                                                                                                                                                                                                                                                                                                                                                                    10416"
                                                                                                                                                                                                                                                                                     family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                    family="Rf:ATR0062|AF013294 T18A10 repeat 1 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="AT_rich"
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. .12282,12422. .12498,12566. .12647,12995. .13077,
. .13236,13328. .13456,13617. .13726,13904. .14249,
                                                                                                                                                                                                                                   family="Rf:ATR0062|AF013294 T18A10 repeat 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0724. 11027,11107. .11799,11889. .11977,12056. .12125
.12282,12422. .12498,12566. .12647,12995. .13077,
.13236,13328. .13456,13617. .13726,13904. .14002)
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Query Match
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GATTGTATCTCCCGATATCGATCTGTCTCGATCATTAGCTCAAAGAGAACAAGACGGCA
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                                   TTGCATTAATACTCATCTCCAATCTCTTCTGAAG 534
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                                                                                                                                             ATTGTGTGGCGATCCGTCTCGATCAACGGCGATAGTGTGTCGATCCGTCTCAATCGACGG
                                                                                                                                                                                                                                                                                                                                                           195;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"

complement(21993. .22079)

/rpt_family="AT_rich"

complement(22194. .22243)

/rpt_family="AT_rich"
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21865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(20454. .20480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="T6B13.6; predicted by genefinder"
complement(join(<19154. .19369,19863. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(19154. .22414)
/gene="At2g14700"
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18635. .18671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSLKFGLLLVVSSDLLLCLVLRAVWEDSRSLSSSTGCCAQMFEFVVGWGFATRLLLRL
VRLRVPERTLFLSWEAIGRVVNISTIAWLVIDEAVECASKKTSYGLSYETHSNLRVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="AAC69372.1"
/db_xref="GI:3810590"
/translation="MAAKTPVKDMADEEGLSFFVSSPIEMSFVEGSTTIATLYFSGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (19154.
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71.2%;
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ement(1915'
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Pred. No. 8.6e-22;
0; Mismatches 68
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RESULT 11
AC005957/c
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VERSION
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                                                   ORGANISM
                                                                                                  AC005957
AC005957.3
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                    HTG.
                                                                                                                                                    Arabidopsis
                                                                  Arabidopsis thaliana.
                                                                                                                                     sequence.
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thaliana chromosome
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T15J14 map mi398, complete
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-FBB-2002) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@tlgr.org On Apr 18, 2002 this sequence version replaced gi:6598502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shen, M., Ro
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Rounsley, S.D., Lin, X.,
Shen, M., Ronning, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Town, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AT_rich" complement(1836..1867) /rpt_family="AT_rich" complement(3450..7066)
                                                                                                                                                                                KVSYENTTDSAVQKAPLQSSQSTYPTTSASKGKSAAASQQNGATEKSLGEKQQNGATK
GKSGHNSSIQVSAAKGSESAGTIAKSLGEKQPTVVPKSHVKKTQLASQTALRRSPRQK
                                                                                                                                                                                                                        LKVWVKŠRTKKYGTPKKĀĀĒIVSSGPQSNGTNEAQDSLSQLLGPDNPSRLRAMGRNMN
KTKLĀCFQVKSKCMĀĒMQOKODOLQQKVNĒLDĒVI DKI KNHVNYTCLLMHKANGSRQSA
EVGĒTŠAĀRSVNGGSOPKCILMŪMAGTDATVVEGCI ISSDĒDĒIVNGSRLĀEPTDVXVL
IDTAIVPĒAYLMRPAINMEIMĒKAVGQMIAMPVAMCVSLĒKLNPĒDIAQSFVAMPAH
                                                                                                                                                                                                                                                                                                      /translation="MASQAKQVFFLREDDSSSWHVAMRGPSRRFREKENDDVTLDIGP
LPTTVDIDVDLEKKKGGQPKKAAATKCNDEVEYUGTLEPTAVEGTVUPVENLEEVED
LDGETEKEAAEDINGETEKEAEDINGETEKEADEDINGETENEAEDINGETENEAEDINGETENEAEDIA
AEEPEGELELSGDEDVOPKTKRQRGPTRMKDIAKDPNARVRVEYTMMGEFICKGSVK
LASYAGALVREHVPITINRWTKIGEBIRTLLMKSVQAKFELDEEYQKVAVLKQMGCLW
RSWKSRQVTKFREAKTNQQRMNLRPKNVSPFEWRKFVKSKTSPEFKKIGSADPTEVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement join (3450. .3728, 3810. .4172, 4473. .4769, 4847. .4885, 4927. .5217, 5452. .5532, 5790. .5993, 6080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(<3450..3728,3810..4172,4473..4769,4847..4885,4927..5217,5452..5532,5790..5993,6080.
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/rpt_family="AT_rich"
    complement(join(<7749. .8219,8355. .8663,8888. .>10105))
                                                                                                                                            TAVWRPSDEIEYMRDSLGSSIAWPKDKLVTY"
                                                                                                                                                                 TSEGLKANQKCKLMDISGKKRVVGAGRVHSIDPDQKVHHVRLGENAARVWVDVVNVDD
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                                              /gene="At2g14980"
/note="mire"
                                                                                                                                                                                                                                                                                                                                                                                                                           /product="En/Spm-like transposon protein"
/protein_id="AAD03355.1"
/db_xref="GI:4115353"
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/note="mis"1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g14970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="overlap with BAC clone T26120
(AC005396:75170. .85214)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="At2g14970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="T15J14.1; related to En Spm transposon family of
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Fraser,C.M., Somerville,C.R. and Venter,J.C.
                                          related to En
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                                       Spm transposon family of
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complement(18558. .18615)
rpt_family="(A)n"
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complement(15639..15677)
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complement(15051. .15)
                                          complement(26681
                                                                                 complement (25946.
                                                                                                complement(25525. .25554)
/rpt_family="AT_rich"
                                                                                                                   /rpt_family="(CAT)n"
complement/25555
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complement/15000
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complement(26681. .27683)
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/note="T15J14.3; pseudogene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16934
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.14984)

(80661

reverse transcriptase"

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sequence - a consensus. from T23015 64288 to
nt, also present in intron 8 of Arabidopsis
for sulfate transporter GB AB012047"
complement(14535, .14596)
                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AT_rich"
complement(13175. . 13)
/rpt_family="AT_rich"
14726. .14753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFERYMKVLKDFVRNTARPEGCIAECYLAEECIQFCSEFLKKTTKVQEKADRNTEYEN
NSILGGRPISAGTFISLTEMERKIAHLAVIQNMAVVEPYVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRVIDMEQLLEIEAEIVETLCLFESFFPPSFFDIMVHLTVHLGREALLGGPVHFRWMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIRKDLHPQTKGKRTYLPAALWSLSKSEKKLFCKRLFDFKGPDGYCSDIARGVSLEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFSRKHVYMGHRMGLPPSHRFRNKKSWFDGKAEHRRKSRILSGLEISHNLKNFQNNFG
NFKQSTRKRKQPESDLPVRHNLDVMHVERNVVASIVSTLMHCGKSKDGVNARKDLEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFRLKTKNGWSDKSFNDLLETLPEMLPEDNVLHTSLYEVKKFLKSFDMGYQKIHACVN
DCCLFRKKYKKLQNCLKCNASRWKTNMHTGEVKKGVPQKVLRYFSIVPRLKRMFRSEE
MARDLRWHFHNKSTDGKLCHPVDSVTWDQMNAKYPLFASEERNLRLGLSTNGFNPFNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(7749. .8219,8355. .8665,8888.
/gene="at2g14980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDNGEWTYDAFSKSSFTLKAMLLWTISDFPAYGNLAGCKVKGKMACLLCGKHTESMWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAD03356.1"
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/translation="MVQLGEIAERDDKKEDELLAKLVDAETPLYPSCVNHSKLSAIVS
                                                                                                                                                                                                    rpt_family="Rf:ATREP4|ATREP4 An AT-rich repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="En/Spm-like transposon protein"
/protein_id="AAD03356.1"
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 177; Conserv
                                                                                                                                                                                                                                                                                    TETETETECCGACATAGATCTGTGTCGATTGTCAGCTTGAAGAGAACAAGACGAGTTG
                                                                                              ATCTCCAATCTCTTCTAAAGA 17970
                                                                                                                                                                                                                                                                                                                                                    TTATTTTTGGCATTCGCGTATTTGGTTTCTCTCTTCATCGGAGAGTCCGACGGCGATTGT
                                                                                                                            ATCTCCAATCTCTTCTGAAGA 535
                                                                                                                                                           TCCATCATCGATCCAAATCGGAGAGTTTGAAGTTCGAAATCGGAGAATTTATTGATACTC
                                                                                                                                                                                        TCCGGTTTCGATCCAAATCGGAGAGTTTGAGGATCTAAATCGGAAATTGCATTAATACTC 514
                                                                                                                                                                                                                           TGTGG---
                                                                                                                                                                                                                                                       CTGTCAAAACGTTAACGATCCGACTCGAGCGTCGACAGTAAGAGAAGAAGACAGCGATTG 394
T32B20 81877 bp
Arabidopsis thaliana BAC T32B20
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complement(join(26960. .26979,27194. .27312,27485.
/gene="At2g15000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich" complement(36100..36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(37029. .38609)
/gene="At2g15020"
/note="T15J14.6; predicted |
complement(<37029. .>38609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative thionin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mawrnagsaarsfysatarspstrspttalprlrpposslpsrr
ftfsspsrnlgalgctosflplysyvatsoltshlnvnlrafcelsngigkdg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="expressed protein"
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/db_xref="GI:20197493"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MEGKTVIFSVLVMGLVISQIQVEAQKTCCPSQSTRKEFEDCISE/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'SGKVNVAVERCTKACSTICTKGSKTAVETV"
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1. .36253
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Pred. No. 9.1e-18;
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                                                                                                                                                                                                                       -CGATCCGTATCCATCGACGGCGATAGTGTGTCGA
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                 linear
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JOURNAL
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AUTHORS
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AUTHORS
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ORGANISM
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AF262041.1
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Washington University Genome Sequencing Center.
The A. thaliana Genome Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, as in preparation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-MAY-2000)
University, 4444 Forest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICE: This sequence may not be the entire insert of this clone may be shorter because we only sequence overlapping sections ce, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 81877)
                                                                                                                                                                                                                                         /gene="T32B20.f"

join(3511. .4334,4377. .44
6605. .7632,7686. .8304)
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EEADSWRSRYERNFGSSRCPAEYRYDLAVHFLEGDAHLMWRSYTARRRQADMSWTDFY
                                                                                                                                                                                                                                                                                                                                                      /clone="T32B20"
3511. .8304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from more than one m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e-mail: rwilson@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Department of Genetics, Washington
St. Louis, MO 63108, USA
                                                                           /product="Hypothetical protein T32B20.f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by:
                                                                                                                                                                                       /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                           /map="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .81877
                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Genetics, Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subclone
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                                                                                                                                                                                                                                                                                                 .4852,4928.
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Missouri 63108, USA
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EAHVLFDSGASHCF1TPESASRGN1RGDPGEQLGAVKVAGGQFLAVLERAKGVD1Q1*P* QPAVQHGAQVQQGVQQLAHIAAAPQGYTTREIGGTSNRAITGFLAHEVCVETLLVGGV SQYATKAALVETAAEVEEDLQRQEVGVSPAVQPKKTQQQVAPSKGSKPAQGQKRKWDH AEFNAKYFAQEALDRMEALFLELTQGERSVREYDQEFNRLLVYAGRGMEDDQAQMRRV

PSRAGQGGRAGCESCGSLDHKVADCTQRAETRECYHCRERGHLRPNCPKLQRMAVTVV

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VAKSKDDGHJDRFLQKIVDDVHACETFPWGRFTFDGCMEGIKVIMNMKGKAKDISSI'
VEXDVYDEKIGFIDLVVDSWRTRLIKEKKKIWWKDMFDHDVRSRSDQOMEEQHISENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(22005. .23540)
/gene="T32820.e"
complement(join(22005. .22139,23232./gene="T32820.e"
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QVNYKTVDHLASVWCEMAEMELRHKNEKGALELLMRAATAVTEVRRRVAADGNEPVO
MKLHRSILRIASFYVDLEESLOTLESTRAVYEKILDLRIATPOIIMNYAFILEENKYE
DAFKYYERGVKIFKYPHYKDIWYTYLTKFYKRYGKTKLERARELFEHAVSMAPSDAVR
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VKAEHQVPGSMLQSLPIPDWKWDFITMDFVVGLPVSRTKDAIWVIVDRLTKSAYFLAI
RKTDGATVLAKKYVSEIVKLHGVPVSIVSDRDFKFTSAFWRAFQAEMDTKVQMSTAYH
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LNLRQRRWMELVADYDLEIAYHPSKANMVADALSCKLYGAAPGQSVEALVSEIGALRL
CAVAREPLGLEAVDRADLLTRYRLAQEKDEGLIAASKAEGSEYQFAANGTILVHGRYC
                                  PHMLREHNQRLLTIERRQDGENVPPFQEKVNVDVNVEKDVGENVPPFEENDVGDNVPPYEENDVGDNVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAAKEFESELKTEPEESVAESSQVATSNKEEEKKTEVSSSSKENV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence-not_experimental /product="Hypothetical protein T32B20.e" /protein id-"AAF67362.1" /db_xref="GI:7682781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEDEMAALERQLLSTTTPTEPAKDGGRRVGFVSAGVISQSGENEGKPVTGNGEDIELP
DESDDESDGDDHVEISQKEVPAAVFGGLARKRDEDGEEAGEDGAAQKLGALERIKRQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFEVQHGNEDTYREMLRIKRSVSASYSQTHFILPENMMQKDKLLDVEDAKGELKRAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKVVTVRDFSV1FDVYSRFEESTVAKKMEMMSSSDEEDENEENGVEDDEEDVRLNFNL
SVKELQRK1LNGFWLNDDNDVDLRLARLEELMNRRPALANSVLLRQNPHNVEQWHRRV
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ELLVHHANVISGLNVDAIIRGGIRKFTDEVGMLWTSLADYYIRKNLLEKARDIYEEGM
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RFIIYERALKALPGSYKLWYAYLRERLDIVRNLPVTHPQYDSLNNTFERGLVTMHKMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical protein T32B20.g"
/protein_id="AAF67364.1"
/db_xref="GI:7682783"
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ISEIKLSPRYIGPFRIVERVGPVAYRLELPDVMRAFRKVFHVSMLRKCLHKDDEVLAK
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PFGLTNAPAAFMRLMNSVFQEFLDEFVIIFIDDILVYSKSPEEHDVHLRRVMEKLREE
complement(30562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="matsvatlsspppvslpllsssrssffsncftvttrpntrslva
IGRRIRQEPTRKPLTCNALFGLGVPELAVIAGVAALLFGPKKLPEIGKSIGKTVKSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEQAIESGLPHKDVKIMCIKFAELERSLGEIDRARALYKYSSQFADPRSDPEFWNKWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="132B20.g"
join(18637. .20487,20649. .21101,21186. .21635)
/gene="132B20.g"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene≖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(25373.
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"T32B20.h"
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                                                                                                                    CTGTCGGTTTTTTCGGTTCGGGTTTCTCGGTTTCTTCCGAACTCCCAGGCCTAGTTTG
                                                                                                                                                                                                                     TCAAATTAAGTTTGCCGACCGGTTTACTCCTTTCTTAAATGTCAGCGCCGATAACCGAAT 12394
                                                                                                                                                                                                                                                                  CTCAAAAGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAA 219
                                                                                                                                                                                                                                                                                                                     AAACCGAATAAACCGATCGGTTAGTGTCTGCCGAACCGTACCGAACCGTTAACCGAAATC 12454
AP002068
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/gene="T32B20.b"
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DDGESTTACGVSVSSPPNVPVDSEEYRAFLKSKLNLACAAVAMKRGTFIKPQDTSGRS
DNGGANESEQASLASSKATPMMSSAITSGSELSGDEEEADGETNMNPTNVKRVKRMLS
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/gene="T32B20.c"
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afdydnggyvtifggelyggngvndepiieetncyeeamenadsrifeeansveeame
navidnrehydsrmbseedngydgribyyelscagershssokvrvlrngkmgrglky
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LLIVAVYVDDLLVTRSSLRMILEFKKEVSTKFEMSDLGRLTYYLGIEVLQHENGIILS
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YLKDYILLSELEGERLRLAIDEEPWDFSEAMELKEWREACREEISSIEKNRTWNLVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANRARNRLYKVTLEVKQNKCLQLSMSSDSMNWHDRMGHIGFDNMKTVINKELVIRIPK
LIVEKQTCTSCLLGKQVRQSFPQSTSYRASNPLELVHGDLCGPITPPTTANKSFGVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRKALEENSDFKDMWYLDNGASNHMTGNLEYFSKIDKTVTGKVRFGDDSRIDIKGKGS
IPFVSKNGDSKLLEDVYYIPDLRSNIISLGQATEAGCDVRMRKGYLTLFDREGELLIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKKY IHLIAALEQVLDVNTLGFED I VGRLKVYEERTCDEDDQGKLMLRTLK I NRTQTV
GEVVDPTEGEEDEVVMED I VIDLKLLKLQETQESENGDTQQADALMMHELVY I NEKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Hypothetical protein T32B20.i"
/protein_id="AAF67366.1"
/db_xref="GI:7682785"
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KGKALIGCKMNRTASMRRVESLEHLQKRIRSVGDQ"
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/protein_id="AAF67360.1"
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/protein_id="AAF67361.1"
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70.2%;
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.36010))
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| CDS | CDS | FEATURES source | | REFERENCE AUTHORS TITLE JOURNAL COMMENT | ORGANISM ORGANISM REFERENCE AUTHORS TITLE TOTRNAL | DEFINITION ACCESSION VERSION KEYWORDS |
|---|--|--|-------|--|---|--|
| CHR" complement(join(21252826,29092991,30663638, 40685540,56526138)) /note="gene_id:T803.2" /pseudo /codon_start=1 /evidence=not_experimental /product="transposon protein-like" complement(join(1017610508,1055110817,1092811178, 1122112021,1212212617,1270413313,1341214198)) /pseudo /codon_start=1 | Complement()oin(8271073,13601604)) complement()oin(8271073,13601604)) /note="gb AAF06086.1 gene_1i:T803.1 similar to unknown protein" /codon_start=1 /evidence=not_experimental /protein_id="BAB01980.1" /db_xref="GI:9294129" /translation="MTRPPIVSGRSTVRGTNFESTSTSYTGLQRPLVPQISNAQAAYI /translation="MTRPPIVSGRSTVRGTNFESTSTSYTGLQRPLVPQISNAQAAYI FALKGMYSLAKSKGKQSEWILSEHWRVMLDYWMTPKAKAKSEKARSSRLESRDGLGAH TRLKGMYSLAKSKGKQSEWILSEHWRVMLDYWMTPKAKAKSEKARSSRLESRDGLGAH | This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is F8N14 and the 3' clone is F1M23. Location/Qualifiers 1. 54386 /organism="Arabidopsis thaliana" /strain="Columbia" /chromosome="3" /clone="T803" /clone="T803" | | 2 (bases 1 to 54386) 2 (bases 1 to 54386) Nakamura, Y. Direct Submission Submitted (16-MAY-2000) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) Tel:81-648-52-3935, Fax:81-438-52-3934) Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=T803 Genes with simllarity to profeins in the databases are described in | , b, t, | thaliana genomic DNA, chromosome 000014 GI:8051676 |
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/note="gb|AAF18641.1
gene_id:T803.8
similar to unknown protein"
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terpene synthase"
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22735...22934,23012...23141,23223...

23626...23722,23887...23952))

/note="gene_id:T803.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(19768. .19837,19928. .20012,20096. 20385. .20434,20533. .20587,20666. .20803,20987. ./note="emblCAB87733.1"
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/product="helicase-like protein"
complement(join(15838. .15949,16034.
16512. .16827))
                                                                                                                                                                                                                                                                                                                                                            gene_id:T803.11"
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35905. .37542
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/note="gene_id:T803.4
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.23310,23406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCAAGCCTACT 29558
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                                                                                           Vysotskaia, V.S., Schwartz, J.R., Yu, G., Toriumi, M., Lenz, C., Li, J., Kremenetskaia, I., Luros, J., Ngan, I., Gonzalez, A., Al Araujo, R., Chao, Q., Conn, L., Conway, A.B., Dunn, P., Hansen, N. Huizar, L., Kin, C., Palm, C., Rowley, D., Shinn, P., Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A.
                                                                                                                                                                                              Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 96183)
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Arabidopsis thaliana chromosome
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                   Theologis, A
                                                       Unpublished
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complement(51010..51506)
/note="gb|AAF24522.1
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EVGEVTGGMDDFALYSFIAMEDCDEKPLYEWFDSKPKILQALSVLYRINNDIVTYERE
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DLTLLKFGKLSFNYCRLHYIQELKTLTKWWKDQDIPSNLPCVRDRIVETYFPTLGLYF
EPRFSLGRIIIAKMTIIVALNDVCDSYATYPEAKSLIDSLQRWDIEAIDELPNYSRI
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9442 c 8904 g 18214
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60.1%;
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                                                                                                                                     Hansen, N.,
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Street, Albany, CA 94710, USA
4 (bases 1 to 96183)
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St., Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theologis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Street, Albany, CA 94
3 (bases 1 to 96183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases
                                                                                                                                                                                                                                                                                                                                        /gene="T518.2"
4184. .6733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="T5I8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="T518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to 96183)
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Submitted (11-MAR-1999) Plant Gene Expression Center, Street, Albany, CA 94710, USA
Gene Expression
                                                                                          Expression
                                                                                          Center,
 Center,
 800 Buchanan
                                                                                          800 Euchanan
                                                                                                                                                                                       800 Buchanan
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/note="Strong similarity to gi|2245113 glycerol-3-phosphate permease homolog from Arabidopsis thaliana BAC gbl297343 and a member of the PF|00083 Sugar transporter family."

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gene

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/gene="T518.5"

complement(join(16592. 17013,17112. 17393,17480. 17836. 1816,18248. 18530,18618. 18690,18769. 18948. 119345,19448. 19580,19943. 20157))

/gene="T518.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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/translation="MPPKAKAKDAGPVERPILGRESSHLKIGIVGLDNVGKSTLENTL
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HEGOGLGNNFLSHIRAVDGIFHVLRAFEBADIIHVDDITVDPVRDLETITEELRLKDIE
FVGKKIDDVERSMKRANDKGLKIELBLLQKYKAMLEDGKDVRFGDWKTADIEILNTFO
LLSAKPVVYLINLNERDYQRKKNKFLEKIHAWVQEHGGDTMLPFSGVFERSLADMAPD
EAAKYCEENKLOSALPRIIKTGFSAINLIYFTAGFDEVKCWQIRROSKAPQAAGAIH
EEAAKYCEENKLOSALPRIIKTGFSAINLIYFTAGFDEVKCWQIRROSKAPQAAGAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Strong similarity to
Lycopersicon esculentum and
subtilase family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(16592. .20157)
/gene="T518.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(7204 .7302,7499 .7549,7870 .7962,
8157 .8232,8340 .8456,8616 .8680,8999 .9112,9212.
9472 .9563,9891 .10014,10118 .10285,10619 .10705))
                                                                                                                         YAGEGVVIGFIDTĞIDPTHPSFSDKISGHTYSVPPHFTGVCEVTIGFPPGSCNRKLIG
ARHFAEALSKGVLNSSQDDASPFDGEGHGTHFASVAAGNHGITVVVACHRLGNASGM
APRAHIAIYKALYKRFGGFAADIIAALÜQAAQDGVDIINLSITPNRREPGIATFENEI
DMALLSAVKAGIFVVQAAGNTGPAPKSMSSFSPWIFTVGATSHDRVYSNSIILGNNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSRAFGGFERLDTFFPFDFCLLKMSSSYISPNFNFWSMVKTTYGEDGDEELCDEVIVN
GDADSAEEPDDDVELDSEMNTMSTTPKHSFMRETERLLKMPSRIRPSTSPPESFLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYKTKFSQFLMFYACSLDPENCGVRFASKLLDIYLSSNTCRLTRMSAVAYLASYLSRG
KFLPASFVASMLKRLVDECAEYCGTCNDDVKPEAHQVFYSGCQAILYVLCFRMRSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSSIGEVVGSVILMMYMERMLDLDLVSGCDDSNGGMFDMELEDAVESTMNEGDEFPVG
ALKQNTSGGNVVSELLDKLMVLFFHHLESCQNSDRLDEVWHQMVFEILFKSFENYILN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:4587515"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(11227. .11491,11761. .11945,12058. .12171
12359 .1246,12540. .12623,12733. .12839,12956. .13024,
13106. .11246,11427. .13516,13598. .13708,13801. .14073,
14128 .14196,14308. .14379,14468. .14551,14659. .14775))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(11227. .14775)
/gene="T518.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SARCLHYLHTGSERGIIHRDVKTTNIILLDENFVAKMSDFGLSKAGPSMDHTHVSTAVK
GSFGYLDPEYFRRQQLTEKSDVYSFGVVLFEAVCARAVINFTLEKDQIIHLAEWALSWQ
KORNLESIIDSNLRQAVSPESLEKYGEIAEKCLADEGKNRPMMGEVLMSLEYVLQIIHE
AWLRKONGENSFSSQAVEEAPESFTLPACSNODSSETEQSQTGSALHNSA"
                                    ALLRYYNSSLLRENGSGKIVGSASVAKIVGGMRPTYGITAPKVMYFSARGPDPEDDSF
                                                          IPGVGLASGTRIMHKLVLATHALRNGTTVMDAIYVGECQDSSSFDQKLVQGKILVCSY
TVRFILGVSTIKQALLTAKNLTAAGLVFYIDPSATGFQMTSSPMDIPGILISSPQDSQ
                                                                                                                                                                                                                                                     PSVHFSGRESSDSKHSLTATSSQIYRTLNRSASIIRVHDSLLRNVLRKENYLKLYSYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKKMQEVHPRVHAALHKISYLIPLAPWNLVSILAQNMRKIDKKDPSIVTYVDNLLRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMDALVDLIISLRITFCVFVVSHHEAATSGKYLDPCLNMLVRNFSQPTFKHKVSQTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comes from this gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(7204. .10705)
VDADIMKPNLVAPGNAIWGAWSPLGIGTNDFQGERFAMESGTSMSAPHVTGIAALIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="T518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="EST gb|Z37678 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb|U80583 proteinase TMP from is a member of the PF|00082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST gb/AA597331
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                                JOURNAL
REFERENCE
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AC009526/c
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Best Local S
Matches 121
   AUTHORS
                                                                                                                                                                                                                        AUTHORS
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                                                          Walker,M.,
Unpublished
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CDS

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MPEWQFSKAIRSAKIRYTDYTWMRLIHFLGKLGNWRRVLQVIEWLQRQDRYKSNKIRI
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30747. .33221
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GNPKQEMVRYQRVSDTSRGIERGSKGDGLDLLAEERRIERLANERHEIRSSKLSGTRR
IGAKRNDDDDDSLFAMETPAFRFSDESSDIVDKPATSRVEMEDRIEKLAKVLNGADIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVATDLKWSKSGESSVALKLSKSGESSVTVPEDESFRKRYSKQEYHRSSDTSRGIERG
SRGDELDLVVEERRVQRIAKDARWSKSRESSVAVKWSNSGESSVTMPKDESFRRRYSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALDPGLIFDIGYNEYMKFLCGINGSSPVVLNYTGESCSSYNSSLAASDLNLPSVTIAK
LVGTRAVLRWYTNIATTATNETYIVGWMAPDSVSVKVSFAKFTIGNGQTRVLSLVFRA
MKNVSMASFGRIGLFGDRGHVVNIPVAVIYKIAV*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLNSKVMFCLNLNTKEVGLQKPGDKGFEFKPSFDQYLQIMESVKTARKKKKFDRLKVE
EDDGGGGNGDSVYEVKDMKIKSGELKDETFRKRYSRQEIVSDKRNERVFKRNGEIENH
                                                                            KERFFRKLEKGDHISAISSLADLNGKIEETELRAFSTSAWSRVLSRFEQDSVLRLMDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(21927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="T518.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MAVTISTNAFVNASLLDESRNSFWRPLFHQPYYNCRRVVRLNSr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 24366
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5,24452. .24542,24632. .25305,25421. .25768)
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Similarity 3.68; 0; Score 87.4; DB 8; Pred. No. 3.5e-12; D; Mismatches 56; 56; Length 96183; 0; Gaps 0

ATTATAATTTTGCCGATCGGTTTAGCCTTCTCTTCATAGTCGGTAATCGGAACCGAAAAA 15307 CAAAAGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACT 221

GTCGGTTTTTTCGGTTCGGGTTTCTCCGGTTTCTTCCCGAACTCCCAGGCCTAGTTTGG 278

15306 ATCGGTTTGTTCGGTTTGTTCGGTTTAATCCGAAATCCCAGGCCTAGTTTCG 15250

gene

AC009526 AC009526 108061 bp Arabidopsis thaliana chromosome AC009526.4 GI:7523676 I BAC

DNA F2J6

genomic linear

sequence, PLN 07-APR-2000

Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Arabidopsis thaliana Eukaryota; Viridiplantae; Arabidopsis thaliana. (bases 1 to 108061) Yu,G., Ecker,J., Theologis, A. and

Dunn, P.,

(bases 1 to 108061)

Federspiel, N.A., Palm, C.J., Altafi, H., Araujo, R., Huiza: Huizar,L., Conway,A.B., Con r,L., Rowley,D., Conn,L., Hansen,N.F)., Buehler,E., Dunn Dunn, P.,

N. M. C.

| gene CDS | gene CDS | gene CDS | COMMENT FEATURES SOURCE | REFERENCE AUTHORS TITLE JOURNAL | REFERENCE AUTHORS TITLE JOURNAL | TITLE JOURNAL |
|---|--|--|--|--|---|---|
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| gene | gene CDS | | gene CDS | | gene CDS | gene CDS |

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TGELERKVQTLQNEATTLSAQVTMLQRGTSELNTENKHLKMRLQALEQQAELRDALNE
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COMPLEMENT (47997. . 49751)
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FYIHCDGALFGLMMPFVKRAPKVTFNKPIGSVSVSGHKFVGCPMPCGVQITRMEHIKV
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ETTTQITFIRVKVRIDFIEPLRFFRRVRFESREGAMNGFNYEKLQQVCTNCCRVNHQV
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protein motif."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(42764. .43362,43458. .43590,44048. .44132,44221. .44429)
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VPPKWTPEEYMTCALPPSSSEKDSEVNQPKPVQHAPLVDCIRTRWSRAACSWSGDPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(39054. .39133,39234. .39345,39452. .39628,40186. .41001)
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Search completed: May Job time : 5656 secs
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Best Local Similarity 62.6
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                       92571 TGGTGTGCCTCTAAACCGAGAAAACCGATCGGTTTAGCTCGCCGAACCGAACCGAACCGT 92512
                                                                                                                     92391 CCTAGCTTTATCCATTAAAACATGTGTTGGTCTT 92358
                                                                                                                                                                                                                                                 92451 GAGAACCGAAACATTCGGTTTTCTCGATTTGGTTTTCTCGGGTTAAGCCGAAATTCCAAG 92392
                                                                                                                                                                                                                                                                                  209 GAGAACCGAAACTGTCGGTTTTTTCGGTTTCCGGTTTTCTTCCGAACTCCCAGG 268
                                                                                                                                                                                                                                                                                                                                                                                                          149 AAACCGAAAATCCTCAAAAGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCC 208
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                                                                                                                                                            CCTAGTTTGGTTTTATTTTTCACGAGTTTTTGCTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTEALKHPGWTAAMHEEYDNCQEAQTWSLVPYTPDMNVLGSKWVFQTKLNADGSLDKL
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VVRYHMSQFYYDADFADVMTETNINNRDFDYDLDDKEATEITDGEHITQIGDNVANML
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WVAVKKLVALQEAIVRSLALTSFPGLLRSSRLSLAALLKQRTDHFQKLLKK"
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DCSPMPTPLPLQLNKVPHQEELFSSPTYFRSLVGKLQYLTLIRPDLQFSVNYVCLKMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WENQIEPYCTVITLFPHNKNRGYHSDPYMRDKCGLYKISGTEKCLLKELIEYIYDNIE
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db_xref="GI:7523685"
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Pred. No. 8.4e-12;
0; Mismatches 80
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Minimum DB :
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                                                                                       Score
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Gapop 10.0 , Gapext 1.0
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2396
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  25.5
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AV556975
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AV548305 AV548305
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AI727861 BNLGH1932
                                                                                     Description
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| 42. | 45. | 48. | 249.6 | 54. | 25 | 58. | 266.4 | 68. | 70. | 72. | 79. | 79. | 28 | 296.2 | 297 | 99. | 99. | 304.6 | 05. | 313 | 16. | 317.8 | 20. | 322 | 22. | 23. | 29. | ω 5 | 348.2 | 5 | 52 | 5 W | 77. | 21. | 40 | • | 20. | N |
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| 14 | 12 | 17 | 14 | 10 | 17 | 12 | 10 | 14 | 14 | 12 | 10 | 12 | 14 | 12 | 14 | 9 | 12 | 14 | 10 | 13 | 14 | 14 | 14 | 14 | 13 | 14 | 12 | <u>_</u> | 10 | 4 | 12 | 9 | 14 | 10 | 10 | 12 | 10 | 10 |
| Q11793 | 49 | L77057 | 185 | 31671 | 5926 | 9600 | BE472133 | 6922 | 6135 | 4488 | 3228 | 8109 | _ | 9551 | დ86199 | 99 | G44899 | 6 | E35416 | 0592 | 6217 | 0462 | G. | 7048 | 2015 | 6649 | 8531 | 7043 | BE343139 | 1866 | 14513 | 2480 | 1866 | 60 | V78875 | F27220 | V8164 | AV788403 |
| Q117934 EST6035 | 61 NF083B1 | 70575 Arabido | ATTSOE | NF064G1 |) Arabido | 8 su79f09 | EST4169 | 0GD5I13 |) QGC18E22 | GA_Ea00 | 'EST3581 | EST48282 | EST60350 | . EST49418 | 861999 QGC1f02. | 00 | 448990 NI | QGD7A12. | ĬĬ. | EST58025 | QGC20F15 | 0665 | 3 QGC17C09 | 7(:484 QGD9C23. | 4 sak89f06 | 65497 QGC8 | 85318 EST48708 | 70439 QGD9A23. | 3139 EST3 | 18665 EST60424 | 445135 GA Ea00 | 042480 24833 CD4 | 118666 EST6 | V796045 AV79 | V788756 AV78 | 272204 GA_ | 816420 AV8 | AV788403 AV788403 |

ALIGNMENTS

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REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AV826684 LOCUS COMMENT ACCESSION DEFINITION TITLE JOURNAL Large scale analysis of Arabidopsis full-length cDNA (2002b) unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Email: mseki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh.M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. AV826684 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-06-F07 5', and Shinozaki, K. AV826684.1 mRNA sequence. thale cress. (bases 1 to 621) GI:19868744 EST 01-APR-2002

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AV548305
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/db_xref="taxon:3702"
/clone="RAFL09-06:F07"
/clone_lib="RAFL9"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The First Laboratory for Plant
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba
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ilarity 100.0%;
Conservative
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/tissue_type="roots"
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/clone="RZL51d11F"
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/strain="Columbia"
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                               CCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTG
                                                                                                 AGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCCGGCACCAAACTGAC 2072
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                                                                                                                                                                                                                                                                                                                        AACTCAACTTTTGGATTCTACAATGAGTGCTGGAAGGAGTTCTACTTGCTGGTGTTCCTGG 2012
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AGTATACTGTTTTTGCATATAGACTTGGGTGCTAAATTTCTTGGTGTAAGCATTTTTATAC
                                                                 CCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTCACCAAGTTCGGTTG 2252
                                                                                                                                     TTGCCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCA 2192
                                                                                                                                                                     CCAGGCATGGAGTTCGCACAATGTTTTGGCCTTGTTGGTGAGAGAAGATCCACATGGCGT
                                                                                                                                                                                                                                      AGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCCGGCACCAAACTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                               486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries DNA Res. 7, 175-180 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Erika Asamizu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/clone="$Q057f09F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
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/strain="Columbia"
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1934

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JOURNAL
                                                                                                          Query Match
Best Local
                                                                                    Matches 474;
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                    1874 GAGAAGCTATGTTGAGGATCAGAATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTC 1933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, Turner, C., Krikorian, S., Elder, L. and Hanson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701516116 A. thaliana, Columbia Col-0, inflorescence-2 Arabidopsis thaliana cDNA clone 701516116, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: service@genomesystems.com
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4633 World Parkwa;
Tel: 877-577-2733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Systems, Inc., a wholly owned subsidiary of Incyte
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                                                                                    Conservative
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                                                                                                                                                                                     from Arabidopsis thaliana, Columbia Col-0, at 4 - 7
weeks. Plants were grown in 1:1:1 peat
moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C
under constant light, and watered with fertilizer. cDNA
synthesis was initiated using a NotI-oligo(dT) primer.
Double-stranded cDNA was blunted, ligated to SalI adaptors
, digested with NotI, size-selected, and cloned into the
NotI and SalI sites of the pSPORT vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
/clone="701516161
                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="inflorescence"
/dev_stage="4 - 7 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="A. thaliana, Columbia Col-0, inflorescence-2"
                                                                                                                                                                                                                                                                                                                                                                  library was derived from untreated inflorescence tissue. from Arabidopsis thaliana, Columbia Col-0, at 4 - 7
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                                                                                                        Score 473.4; DB Pred. No. 2e-105;
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REFERENCE
AUTHORS
TITLE
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GCCAAATGCAGGGCTTGTGTGTGAGTACAAATGCACGGTTTTACGCGATTGTGAAGCCAAT 809
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AV547260 Arabidopsis thaliana roots Col
CDNA Clone RZL28cllF 3', mRNA sequence.
AV547260
AV547260.1 GI:8718674
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                               Conservative
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asamizu@kazusa.or.jp,
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                                                                                                                                                                                       /clone_lib="Arabidopsis thaliana
/tissue_type="roots"
                                                                                                                                                                                                                                    /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                          /note="Vector:
                                                                                                                                                                                                                      /clone="RZL28c11F"
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URL:http://www.kazusa.or.jp/en/plant/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BNI.GH19321 Six-day Cotton fiber Gossypium hirsutum cDNA to PHOSPHOMEVALONATE KINASE, mRNA sequence.
A1727861
A1727861.1 GI:5046713
                                                                                                                                                                                                                                                                             Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Gossypium hirsutum
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                                                                                                                                                                                                                                   Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
                                                                                                                                                                                                                                                                   Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                                                                      /clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"
151 c 144 g 219 t 1
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/cultivar="Acala Maxxa"
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76.1%;
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Pred. No. 1.1e-93;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
          Large scale analysis of Unpublished (2002) Contact: Motoaki Seki
                                                        Seki,M., Narusaka,M., Ishida,J., Kamiya,A.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Arakawa,T., Shibata,K., Shinagawa,A., Murama
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AV788403 RAFL6
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                                                                       Satou,M., Nakajima,M.,
Itoh,M., Ishii,Y.,
                                                         Hayashizaki,Y
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Matches 424;
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                                                                           AV816420
AV816420 RAFL9 A
mRNA sequence.
AV816420
AV816420.1 GI:
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web tite (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
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3-1-1 Koyadai, Tsukuba, Ibaral
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                       Arabidopsis
                                        thale cress
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dehydration (1, 2, 5, 10, 24
hr) treatments"
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/db_xref="taxon:3702"
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and cold (1,
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Streptophyta;

Embryophyta;

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Best Local Similarity
Matches 422; Conserv
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                           AATC 2376
                                                                        CCATTGTAAGGTCTTTAACTCTTGGAAAACTTGCGGGAAAATAAAATAAAGTTGATTTCA 2372
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                                                      CCATTGTAAGGTCTTTAACTCTTGGAAAACTTGCGGGAAAATAAAATAAAGTTGATTTCA 5
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibara Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 424)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
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/clone_lib="RAFL9"
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/db_xref="taxon:3702"
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Query Match
Best Local Similarity 71.8
'--- 550; Conservative
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                   GCAAATTAGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTAGTGTGC 1798
                                                                                                                                                                                                               CACCATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAGGCACGAG
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GAAAATTAGCCAAAGAACACTGGGATGCCTATAAATGCGTGATTGAAAACTGTAGTAGGC
                                                                                             AAACATGGAGAAAGCTGGCCGATGCTAATTCAGAACTTGAGACACAACACAACATGTTAA
                                                                                                                   AAAACTGGCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGA 1738
                                                                                                                                                                                    CACCATCAATGGTAGGTGCTGTTAAAAAAATGGCAGAAGGCTGATCCTGAAAAAATCCCCAAG
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BF272204
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D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm
of the cotton fiber
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GA_Eb0014D16f Gossypium arboreum 7-10 dpa
arboreum cDNA clone GA_Eb0014D16f, mRNA se
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Tel: 864 656 7288
Fax: 864 656 4293
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/clone="GA_Eb0014D16f"
/clone_1ib="Gossypium arboreum 7-10 dpa fiber library"
/clone_tip="Fibers isolated from bolls harvested 7-10
dpa"
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149 c 227 g 22
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/strain="AKA"
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                                                                                                                                                                                              Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
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                                   /clone_lib="RAFL6"
/dev_stage="plants at various
germination to mature seeds"
/lab_host="DH10B"
                                                                                                      /organism="Arabidopsis
/db_xref="taxon:3702"
/clone="RAFL06-80-003"
   /note="Site_1: SstI; Site_2:
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                                                                  Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Genomic Sciences
3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-4359
                                                                                                                                                                                                                                              Contact: Motoaki Seki
Plant Functional Genom
                                                                                                                                                                                                                                                                             Large scale analysis of Unpublished (2002)
                                                    site (http://www
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Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
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   Location/Qualifiers
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Pred. No. 7e-89;
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Hayashizaki,Y

Nakajima, M., Ishii, Y.,

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                                                                           Karamycheva, S.A.
Generation of a set of
                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 844)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
             Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                         Solanum tuberosum
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potato@tigr.org
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/lab host="DH10B"
/note="Site_1: BamHI; S
dehydration (1, 2, 5, 1
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/clone_lib="RAFL9"
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/db_xref="taxon:3702"
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Pred. No. 1.1e-87;
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TGTGCTTACTTCTGAAAAGTGGGTGTTACATGCTACTGAACCAATCAACG&AGCCATTAT
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/lab_host="SOLR"
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/clone="STMEC81"
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67.5%;
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Pred. No. 7.6e-82;
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MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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24833 CD4-16 Arabidopsis thaliana cDNA clone H9F5T7, mRNA sequence
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                                                                                                                                                               /tissue_type="seedling hypocotyl"
/dev_stage="3 day-old"
/dev_stage="3 day-old"
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/dev_stage="3 day-old"
/dev_stage="3 day-old mRNA from 3 day-old arabidopsis thaliana (Columbia) seedling hypocotyls as template and oligo d(t) as primer, first strand synthesis was catalyzed by Moloney murine leukemia virus reverse transcriptase (Pharmacia). Second-strand cDNA was made using the procedure of Gubler and Hoffman (1983) except that DNA ligase was omitted. After the second strand reaction, the ends of the cDNA were made blunt with Klenow fragment and EcoRI/NotI adapters (Pharmacia) were ligated adapters by spun-column chromatography using sephacryl s-300 and size-fractionated on a 1% low melting point mini-gel. Size selected cDNAs (3 - 6 kb) were removed from the gel using agarase (New England Biolabs), phenol:choloroform extracted and precipitated with lug of lambdarant (Statafagener) was co-precipitated with lug of lambdarant (Statafagener)
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               lambdaZapII (StratageneEcoRI digested, dephosphorylated arms and then ligated in a volume of 4 ul overnight. Each ligation mix was packaged in vitro using Gigapack II gold packaging extract (Stratagene). We have determined that although first strand cDNA synthesis was initiated using dT, almost all of the cDNAs begin 8-10 bp from the poly-A
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="H9F5T7"
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Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 693.
                                                                                                            Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., D., Wood,T.C., Leslie,A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evc of the cotton fiber
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                                                                                                                                                                                                                                                                                                                         CCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTT
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                                                                     BQ118665 769 bp
EST604241 mixed potato tissues 5' end, mRNA sequence
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BQ118665.2
                      potato.
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                                                                    mRNA sequence.
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/clone="gA_Ea0026066f"
/clone_1ib="Gossypium arboreum 7-10 dpa fiber libra
/tissue_type="Fibers isolated from bolls harvested
dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI;
177 c 161 g 255 t 2 othe
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Pred. No. 9.3e-76;
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674 ACTCTTTGAAAATGGCTGTTGTTGCTTCTGCTCCTGGGAAGTTTTTGATGACTGAGGGCT 733
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CACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTG
                                                                                                                                                                                                                                                                                                     TACAGTATGCTATAGCTGCTGCTCATTTGGCAACCGAGAAGG---ACAAAGAATCATTGC
                                                                                                    ATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTG
                                                                                                                                                                                ACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGACTTTTACTCAT
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                                                                                                                                                      AGAGACTACTTCTGCAGGGTCTTGACATAACTATCTTGGGTTGCAATGAGTTCTATTCGT
                                                                                                                                                                                                                                                        TGCAGTATGCTGTTGCAGCAGCCCATGCAACACTTGACAAAGATAAGAAGGACACATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available through the Research Genetics, contact Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation of a set of potato cDNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: potato@tigr.org
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/tissue_type="mixed tissues"
/lab_host="SOLR"
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/clone="smwron:"
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Listing first 45 summaries
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| COTGTA | 45A-21 21, Application NFORMATION: TY: FAICO, S. Car TY: FAMOU, OMO! INVENTION: Squ APPLICATION NUMBER FILING DATE: 29 PLICATION UMBER LING DATE: 1998 PLICATION UMBER LING DATE: 1998 PLICATON ON UMBER LING DATE: 1998 PLICATION | 1 |
| 9.6 Similarity 61.3 9; Conservative GTGGTGGATCCTCACA | 45A-21 21, Application US/0990974 21, Application US/0990974 INFORMATION: IT: Fanco, S. Carl IT: Famodu, Omolayo O. INVENTION: Squalene Synth EXERNEE: BB1112 US CIP APPLICATION NUMBER: US/09/ FILING DATE: 2001-07-20 PLICATION NUMBER: 09/433,2 PLICATION NUMBER: 60/107,2 PLICATION NUMBER: 60/107,2 PLICATION NUMBER: 60/107,2 PLICATION SUMBER: 60/107,2 PLICATION OMBER: 60/107,2 PLICA | 3468 1536 455 648 1141 1141 1147 5465 3632 3632 9652 135030 367379 2209 12209 12209 1236 411 5464 601 6264 |
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| tch 9.6%; Score 229.2; DB 6; Length 757; al Similarity 61.3%; Pred. No. 2.3e-52; 369; Conservative 0; Mismatches 233; Indels 0; G GAAGTGGTGGATCCTCCACCACCATCAATGGTAGGTGCAGTAAAGAAGTGGCAAAATGTCTG [| Enzymes 45A | 9 US-10-282-122A-10932 8 US-10-369-493-46489 8 US-10-391-339-5507 9 US-10-991-37-604A-5821 6 US-09-807-604A-58235 7 US-09-837-604A-28235 7 US-09-837-604A-13747 7 US-09-949-016-13747 7 US-09-949-016-13747 7 US-09-949-016-14896 9 US-10-311-455-882 7 US-09-837-604A-164 1 PCT-US02-41115-94 9 US-09-837-604A-164 1 US-09-815-606A-49691 7 US-09-837-604A-10493 1 US-09-949-016-166383 9 US-10-240-452-67 9 US-10-240-452-67 |
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| yth 757; gls 0; G gcaaargrcag gcagaagrcag gragaacrgaaa [| | sequence |
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CURRENT FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 49762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 33093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33093, Application US/60288292
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Norriss, Michael G
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Best Local Similarity
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                                                               GAAATACTCTCCTCGGCTCAGGTTTCAGGAGGATGTTG---CTTGCCAGAAGTAGTAGCA
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 18322
LENGTH: 379
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18322, Application US/10389048
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
APPLICANT: Shenk, Michael A.
                                                                                                                                           Sequence 65010, Application US/09837604A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: De La Pena, Robert C.
APPLICANT: De La Pena, Robert C.
APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51892)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 25129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Polynucleotides, Materials Incorporating TITLE OF INVENTION: Them, and Methods for Using Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 11000.1041U1c1
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CURRENT APPLICATION NUMBER: US/09/837,604A CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: US 60/197,872 PRIOR FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 81288

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                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09909745A GENERAL INFORMATION:
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                                                                                                             SOFTWARE: M:
SEQ ID NO 19
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                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/433,242
PRIOR FILING DATE: 1999-11-04
                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                APPLICANT: Famodu, Omolayo O. TITLE OF INVENTION: Squalene SFILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                                                                                                         APPLICANT: Falco, S. Carl APPLICANT: Famodu, Omola
                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                          TYPE: DNA
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TYPE: DNA
NAME/KEY: unsure LOCATION: (287)
                                                      ORGANISM: Oryza sativa
                                       FEATURE:
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                                                                                                                                 Microsoft Office 97
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Pred. No. 7.4e-33;
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; LOCATION: (533)
; OTHER INFORMATION:
US-09-909-745A-19
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OTHER INFORMATION:
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                                      CTTCTGGATGCCACTATGAATATGGAGGGTGTTCTACTAACTGG-ATTCCTGGGGGCCGGT
                                                              CTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGT
                                                                                        ATATGCCAAGAGATGGGCATAGCAGCTGGTGTTCCAATTGAGCCAGAATCACAAACTCAA
                                                                                                                                         AAGAACTAATTGTTAGATCATTACTGGCCGCAAGAGATGCTTTCCNTGAAATAAGGCTTC
                                                                                                                                                                  ACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTC
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US-09-837-604A-38723/c; Sequence 38723, Application; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 81288
SEQ ID NO 34763
LENCTH: 388
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Best Local Similarity
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Sequence 34763, Application US/09837604A
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               APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                APPLICANT:
                                                                                                APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shukla, Hridayabhiranjan
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated
TITLE OF INVENTION: Plants
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                                                                                                                                                                                                                                                                                                     AATCACAAACTCAACTTCTGGATGCCAC 387
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                                                                                De La Pena, Robert C.
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Shukla, Hridayabhiranjan
De La Pena, Robert C.
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Pred. No. 6.3e-28;
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; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3109-046-Q1-K1-C9
US-09-615-606A-54496
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                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/615,606A; CURRENT FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 91663
SEQ ID NO 54496
LENGTH: 296
TYPE: Page 15.
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CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/197,872
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 81288
SEQ ID NO 38723
LENGTH: 585
 Matches 163;
                  Best Local Similarity
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
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APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules And Other
TITLE OF INVENTION: Plants
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                4.7%;
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Score 113.8; DB 6
Pred. No. 9.2e-21;
0; Mismatches 82
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                                  DB 6; Length
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PRIOR APPLICATION NUMBER: 09/433,242
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
SEQ ID NO 15
SEQ ID NO 15
OFFICE DATE: 249
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                                 RESULT 10
US-09-745A-17
S-09-909-745A-17
Sequence 17, Application US/09909745A
GENERAL INFORMATION:
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
APPLICANT: Falco, S. Carl
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                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 25849
LENGTH: 1269
                                                                          Query Match 3.18;
Best Local Similarity 48.48;
Matches 239; Conservative
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LENGTH: 249
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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SOFTWARE: Microsoft Office 97
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ORGANISM: Zea mays
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  TCAAGTACATAAGACTGGTTTAGGAAGCTCGGCAGCTATGATTACAAGTCTTATAGGTTC 497
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Pred. No. 5.7e-19;
                                                                            Score 73.6; DB 8;
Pred. No. 1.6e-09;
0; Mismatches 249
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                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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equence 25596, A<sub>l</sub>
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1517 GTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTCTCTTTACCACCACTGA 1576
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mes 138; Conserv
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                                                                                   CAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTG 1516
                                                                                                                          GAAGCGGGTTTGATGTAGCGGCGGCAGCATATGGATCTATCAGATATAGAAGATTCCCCAC 670
                                                                                                                                                                 GAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC 1456
                                                                                                                                                                                                             ATAGAGAAGTTATTCATAATTTAGCACAAGTTGCTCATTGTCAAGCTCAGGGTAAAATTG 610
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                                         CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC 730
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Pred. No. 4.2e-05;
0; Mismatches 134;
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US-10-320-797-2218
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                                                                                                             GENERAL INFORMATION
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SEQ ID NO 2218
LENGTH: 1506
                                                                                                                                 Sequence 2218, Application US/10320797
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Best Local Similarity
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                  TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: 10182-021-999
                                                                            APPLICANT: Eroshkin, Alexey M. APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/40225
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
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APPLICANT: Zamuddio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS
TITLE OF INVENTION: METHODS OF USE
  CURRENT
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LOCATION: (1305)...(1305)
OTHER INFORMATION: n=g,
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OTHER INFORMATION: n=g,
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LOCATION: (1285)..(128
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SEQ ID NO 2218

ENGTH: 1506

CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: Patentin version 3.1

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; TYPE: DNA
; ORGANISM: HUMAN
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2556324)
; OTHER INFORMATION: n = A,T,C or G
US-09-947-911-95
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: LOCATION: (1313)..(1313)
: OTHER INFORMATION: n=g, a, t or c
US-10-320-797-2218
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Db 2311111 TTTAGGATAATGATAAACTTTTAGAATTTGTTAATACAATTTTTATAATTGAATATATCA 2311052
                                                                                                                                                                                                                                                                                                                                                 Sequence 95, Application US/09947911
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CLOO1300
CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
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Best Local Similarity 54.9%;
Matches 84; Conservative
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                SEQ ID NO 95
                                                                             Matches
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1311)...(1311)
OTHER INFORMATION: n=g, a, t or c
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1305)..(1305)
OTHER INFORMATION: n=g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Cryptococcus neoformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION: (1285)..(1285)
OTHER INFORMATION: n=g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1285)..(128
                      2250 TTGAGTATACTGTTTTGCATATAGACTTGGGTGCTAAATTTCTTGGTGTAAGCATTTTTA 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003 GTGTTCCTGGAGCTGGTGGATTTGATGCCATAT 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1883 TGTTGAGGATCAGAATTCTTATGCGTCAGATGGGTGAGGCGGCTAGCGTTCCGATAGAGC 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EATURE:
                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1430 GCGTTCCAGGTGCGGGCGGCTACGATGCCCTTT 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1370 CAAAAGAACAAACGAGATTGCTGGATGCATGCGGACAAGTCAAGGGTGTTGTAGGCGGTG 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1943 CTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTG 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1310 TNTNGTCCATCCGCGCTCTGTTGCGTGAAATGTCCGACCTCTCGGGCGTACCCATCGAAC 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EATURE:
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                                                                             Conservative
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P
                                                                           Score 42; DB Pred. No. 8.4; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.8; DB 9;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                              DB 7; Length 2556324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                           65;
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Search completed: May 3, 2003, 20:27:13
Job time: 1891 secs

Db 2310991 TAAAAGCATCCAAATCGTAACAAAAA 2310966

THIS PREE BLANK (USPTO)

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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2396
1 gtcgacccacgcgtc
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17118.898 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | | | | | | | ი | | | O | | | | | O | | | | Result |
|----------------------|----------------------|--------------------|---------------------|---------------------|-------------------|----------------------|----------------------|-------------------|-------------------|---------------------|---------------------|---------------------|---------------------|--------------------|----------------------|----------------------|--------------------|-------------------|-------------------|-------------------|----------------|
| 2 | õ | 9 | <u>6</u> | 17 | 9 | 5 | 4 | 13 | 2 | Ξ | 5 | 9 | æ | 7 | σ | Ų | 4 | ω | 2 | 1 | : |
| 402.2 | 402.2 | 411.2 | 418.2 | 421.4 | 425.4 | 425.4 | 425.4 | 443 | 443 | 454.4 | 463.6 | 473.4 | 486.6 | 518.4 | 569.6 | 569.6 | 759 | 840.2 | 840.2 | 2396 | Score |
| 16.8 | 16.8 | 17.2 | 17.5 | 17.6 | 17.8 | 17.8 | 17.8 | 18.5 | | 19.0 | 19.3 | 19.8 | 20.3 | 21.6 | 23.8 | 23.8 | 31.7 | 35.1 | 35.1 | 100.0 | Query Match |
| 448 | 448 | 457 | 511 | 458 | 728 | 728 | 728 | 443 | 443 | 1887 | 1889 | 475 | 1892 | 1956 | 576 | 576 | 119420 | 1509 | 1509 | 2396 | Length |
| 27 | 25 | 17 | 17 | 17 | 37 | 27 | 25 | 30 | 24 | 28 | 28 | 25 | 28 | 42 | 27 | 25 | 31 | 38 | Н | 37 | DB |
| US-09-684-016-154090 | US-09-654-617-154090 | US-09-333-534-5570 | US-09-333-534-13678 | US-09-333-534-13646 | US-09-988-863A-4 | US-09-684-016-192867 | US-09-654-617-192867 | US-09-770-444-851 | US-09-638-111-871 | US-09-708-427-66288 | US-09-708-427-83406 | US-09-649-165A-2752 | US-09-708-427-65886 | US-10-219-999-9087 | US-09-684-016-121976 | US-09-654-617-121976 | US-09-803-736-1155 | US-10-036-959B-5 | PCT-US02-24048A-5 | US-09-988-863A-1 | ID |
| Sequence 154090, | Sequence 154090, | Sequence 5570, Ap | Sequence 13678, A | Sequence 13646, A | Sequence 4, Appli | Sequence 192867, | Sequence 192867, | Sequence 851, App | Sequence 871, App | Sequence 66288, A | Sequence 83406, A | Sequence 2752, Ap | Sequence 65886, A | Sequence 9087, Ap | Sequence 121976, | Sequence 121976, | Sequence 1155, Ap | Sequence 5, Appli | Sequence 5, Appli | Sequence 1, Appli | Description |
| | | | | | | | | | | | | | | | | | | | | | |

| 241 GTTTCTCGGTTTCTCCGAACTCCCAGGCCTAGTTTGGTTTATTTTTCACGAGTTTGC [| 181 GTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACTGTCGGTTTTTTCGGTTCGG | 1:21 1:21 | | GTCGACCCACGCGTCCGGGCCGACCGACCCGCGTCCGGGCCGACCGA | Query Match 100.0%; Score 2396; DB 37; Length 2396; Best Local Similarity 100.0%; Pred. No. 0; Length 2396; Concernition of the control of th | | 1 2396 Arabidonsis t | CURRENT APPLICATION NUMBER: US/09/988,863A CURRENT FILING DATE: 2001-11-21 NUMBER OF SEQ ID NOS: 5 COFTWARE: Patenth ver 2 1 | ENERAL INFO APPLICANT: TITLE OF IN | RESULT 1 US-09-988-863A-1 : Sequence 1 Application US/09988867A | ALIGNMENTS | 9.6 757 18 US-09-433-242A-21 Sequence 21, A 9.6 757 34 US-09-433-242A-21 Sequence 21, A 9.6 757 34 US-09-97-45-21 Sequence 21, A 9.5 40548 20 US-09-534-859-716 Sequence 716, A | 286 11.9 460 18 US-09-404-520-9784 Sequence 286 11.9 460 57 US-60-138-103-9068 Sequence 247.8 10.3 519 28 US-09-705-926-20673 Sequence 247.8 10.3 517 28 US-09-705-926-20673 Sequence 247.8 10.1 517 28 US-09-705-026-20673 | 307 12.8 1665 42 US-10-219-99-33255 Sequence 302 12.6 1053 42 US-10-219-99-10586 Sequence 302 12.6 1053 75 US-60-312-544-58 Sequence 302 12.6 1053 75 US-60-312-544-58 Sequence 299 2 12.5 611 37 US-60-988-634-3 Sequence | 362.4 15.1 364 25 US-09-654-617-181171 Sequence 181171, 362.4 15.1 364 27 US-09-684-016-181171 Sequence 181171, 362.4 15.0 421 17 US-09-333-534-16350 Sequence 16350, 358.8 15.0 421 17 US-09-333-534-16350 Sequence 16350, 359.8 16-09-705-956-13137 Sequence 16350, 359.8 16-09-705-956- | 383.2 16.0 489 27 US-09-684-016-134754 Sequence 134754, 382.8 16.0 1470 25 US-09-684-617-259014 Sequence 259014, 382.8 16.0 1470 27 US-09-684-016-259014 Sequence 259014, 382.8 16.0 1470 27 US-09-684-016-259014 Sequence 259014, 381 15 9 477 US-09-684-016-259014 | 22 400.4 16.7 840 19 US-09-505-532-46021 Sequence 46021 23 400.4 16.7 840 31 US-09-819-091A-46021 Sequence 46021 24 390 16.3 501 17 US-09-333-534-2389 Sequence 2389, 25 38 2 16 0 480 25 US-00-534-517-14754 Common 12175 |
|--|---|---|---|---|--|---|---|--|---|---|---|--|---|--|--|--|--|
| Oy 1321 AAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTTGTCTT 1380 | Qy 1261 GTTGCAGCTCTGTTACATTATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAGAAGGA 1320 | OY 1201 TCCAAGCCTGAAGTAGCAAAAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTG 1260 | QY 1141 GGTACCCTTGCACCGTTTGCATCACATTCAATGCTGCGGAGTCAAATGGTGCTAAT 1200 | QY 1081 TITTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG 1140 | QY 1021 GAATCATTGCACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGAC 1080 | Qy 961 GTAGAGCATGCGATACAGTATGCTATAGCTGCTCATTTGGCAACCGAGAAGGACAAA 1020 | Oy 901 CTGTCACTGAATCATTTGACTCTTCAGTCTGTGCAAGTGATTGAAGAAACCCCTTT 960 | QY 841 TGGAAATGGACAGATGTCAAATTAACATCACCACAGGTCTCGAGAGAAAGCATGTATAAA 900 | QY 781 GCACGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCA 840 | OY 721 ATGACTGGAGGCTACCTTGTACTCGAGAAGCCAAATGCAGGGCTTGTGTTGAGTACAAAT 780 | Qy 661 GATTATCTTTGTCACTCTTTGAAAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTG 720 | QY 601 TCCGATCATTTCCGGCGATATCCAATCGCAGACTGAGGTGAATCTGGGGTTTTGATCAGC 660 | Qy 541 AATCCGATCTACCACCACTACTCGTACCGCCGGTCATTACTGCCGCCGATTTCAAATTA 600 | OY 481 TTGAGGATCTAAATCGGAAATTGCATTAATACTCATCTCCAATCTCTTGCTGAAGAGTCCG 540 | Qy 421 CGATCCGTCTCGATCGAGGGAGAATACGTTTCGATCCGGTTTCGATCCAAATCGGAGAGT 480 | Qy 361 GAGCGTCGACAGTAAGAGAAGAAGACAGCGATTGTGTGTAGATCGACGGCGAACGTGTGT 420 | Qy 301 TTCTCTTTTCATCGGCGACGACGACGTCGAGTTTCTGTCAAAACGTTAACGATCCGACTC 360 |

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RESULT 2
PCT-US02-24048A-5
; Sequence 5, Application PC/TUS0224048A
; GENERAL INFORMATION:
    APPLICANT: E.I. du Pont de Nemours &
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Nemours & Company

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PRIOR APPLICATION NUMBER: 60/307,63
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 1509
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Matches 1108; Conser
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ORGANISM: Hevea
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                                                                      SEQ ID NO 5
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GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours & Company
APPLICANT: Hallahan, David L.
APPLICANT: Keiper-Hrynko, Natalie
TITLE OF INVENTION: Genes Involved in the Biosynthesis of Isopentenyl Diphosphate
TITLE REFERENCE: CL-1792
FILE REFERENCE: CL-1792
                                                                                                                                                CURRENT FILING DATE: 2002-05-10 PRIOR APPLICATION NUMBER: 60/307,637 PRIOR FILING DATE: 2001-07-25
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/036,959B CURRENT FILING DATE: 2002-05-10
                                                                                                              SOFTWARE: Microsoft Office 97
                                                                                                                                 NUMBER OF SEQ ID NOS:
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| 15 | 73 GISCIIICCICISCICASSAISCISSSAAATAGAACTGAGTTCTCTTTACCACC. | 0 5 | |
| A 1521 | 1462 GTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCATTAAATGAAGTTATTGGTACA | Dy Oy | |
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| 14 | 02 GGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGTTATGTTCGCTTCTCTC | ο _γ ; | |
| T 1401 714 | 1342 GATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAAGGGAAGGTCGGAAGG | P 6 | |
| 65 | 601 CTTGGATTGATCTTTCATCCTCTTGTAAAGAGAAAATTTTCTGATCTT | Db | |
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| C 600 | 541 ACTGGATTGGGTTCATCAGCAGCAGCAACTGCTGCTGCTGCTGCTTACTTCATCAC | Db | |
| r 1281 | CTGGCTT | Qy | |
| A 540 | 481 TCAATCACCTTCAATGTAGAGGAAGCAAATGGACAAAACTGCAAGCCTGAGGTAGCTAAA | Db | |
| A 1221 | CAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAC | Qy | |
| A 1161 C 480 | 1102 ATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTGCA | Оу Дъ | |
| 3 420 | GCAAGGTCTTGATATTACAATATTAGGTACCAATGACTTCTATTCATACCGAAATG | DЪ | |
| 3 1101 | TGCAAGGTCTTGATATAACAATATTAGGCTCCAATGACTTTTACTCA: | Qy | |
| 360 | 301 GTAGCAGCTGCACATGCAACACTTGACAAAGATAAGAAGATGTCTTAAACAAGCTACTC | Db | |
| A 1041 | AGCTGCTGCTCATTTGGCAACCGAGAAGGACAAAGAATCATTGCACAAACTCT | Qy | |
| r 300 | AAGGAACCCATTTGTGGAACAAGCAGTGCAATTTGC | DЬ | |
| r 984 | AGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGTAGAGCATGCGATAC | Qy | |
| r 240 | GGGAAAGCTTGTACAAATTGTCACTGAAAAATTTAGCTCT | Db | |
| r 924 | CACCACAGCTCTCGAGAGAAAGCATGTATAAACTG | Qy | |
| A 180 | CTATTTACGATGAAATCAAACCTGATAGTTGGGCATGGGCATGGACTGAAATT | Db | |
| A 864 | CGAAGAAGTCAAGCCTGAAAGTTGGGCATGGAAATGGACAGA1 | Qy | |
| 3 120 | 61 GAAAGACCCAATGCAGGATTGTACTCAGCACAAATGCTCGATTCTATGCCATTGTGAAG | DЪ | |
| 3 804 | AGAAGCCAAATGCAGGGCTTGTGTTGAGTACAAATGCACGGTTTTACGC | Qy | |
| G 60 | 1 ATGGCTGTAGTTGCTTCTGCTCCGGGTAAGGTGTTGATGACTGGGGGGTTACCTCATATTG | Db | |
| € 744 | TGTTGTTGCTTCTGCTCCTGGGAAAGTTTTGATGACTGGAGGCTACCTTGTAC | Qy | |
| Gaps | Query Match 35.1%; Score 840.2; DB 38; Length 1509; Best Local Similarity 73.1%; Pred. No. 1.9e-207; Matches 1108; Conservative 0; Mismatches 398; Indels 9; G | X m O | |

| 1160 29018 1220 | | o S- | | | | | RESI US-I | Оy | Фр | рь | рь | DB 09 | , dd | р _р | Db Qy | 망 |
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| CATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAA 1219 | Pred. No. 1.7e-185; 0; Mismatches 0; nTTGACACCAGAATCGCTGGGT | is thaliana | NUMBER OF SEQ ID NOS: 1582 SEQ ID NO 1155 LENGTH: 119420 TYPE: DAM | CURRENT FILING DATE: 2001-03-12 PRIOR APPLICATION NUMBER: US 09/534,859 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 | APPLICANT: Rounsley, Steven D. APPLICANT: Wiegand, Roger C. TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof FILE REFERENCE: 38-10(15493)D CURRENT APPLICATION NUMBER: US/09/R03.736 | RMATION: Bush, David F. Levin, Irena M Norris, Susan | RESULT 4 US-09-803-736-1155/c ; Sequence 1155, Application US/09803736 | 2182 TCATCAATTCACCTT 2196 1 1495 TTTGCAGTTCATATT 1509 | 2122 CCACATGGCGTTTGCCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTT 2181 | 2062 ACCAAACTGACCCAGGCATGGAGTTCGCACAATGTTTTTGGCCTTGTTGGTGAGAGAAGAT 2121 | 2002 GGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCCGGC 2061 | 1942 CCTGAATCTCAAACTCTACTTTTGGATTCTACAATGAGTGCTGAAAGGAGTTCTACTTGCT 2001 | 1882 ATGTTGAGGATCAGAATTCTTATGCGTCAGATGGGTGAGGCGGCTAGGGTTCCGATAGAG 1941 | 1822 CATGCTACTGAACCAATCAACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAGAAGCT 1881 | 1762 GATGTITATCTACGAGTCATTAAGTCTTGTAGTGTGCTTACTTCTGAAAAGTGGGTGTTA 1821 | |
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Annotated Plant General Reperence:

CURRENT APPLICATION NUMBER: US/09/654,617

CURRENT FILING DATE: 2000-09-05

NUMBER OF SEQ ID NOS: 463173

SEQ ID NO 121976
LENGTH: 576

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Pred. No. 3.9e
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NUMBER OF SEQ ID NOS:
SEQ ID NO 121976
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CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654
PRIOR FILING DATE: 2000-09-05
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SEQ ID NO 9087
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TITLE OF INVENTION: CDNA SEQUENCES AND USES
FILE REFERENCE: 38-10(527.6)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILLING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, M
APPLICANT: Hinkle, Gre
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LOCATION: (140)..(1675)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea
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Hinkle, Gregory J.
Kovalic, David K.
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LCGATION: 1..1892
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Best Local Similarity
Matches 924; Conserv
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LENGTH: 1892
TYPE: DNA
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APPLICANT: N. ALEXANDROV et
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SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2000-11-09
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NAME/KEY: misc_feature
LOCATION: 1..1892
OTHER INFORMATION: any n
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US-09-708-427-83406
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LENGTH: 475
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                                             APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Guegler, Karl
APPLICANT: Doyle, Martin
           NUMBER OF SEQ ID NOS: 85364
                     CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 7753
SOFTWARE: PERL Program
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CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/150,517
PRIOR FILING DATE: 1999-08-24
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                     Sequence 66288, Application US/09708427
GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND OFFILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND OFFILE REFERENCE: 2750-1243P
CURRENT EILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 66288
LENGTH 1887
             NAME/KEY: misc_feature
LOCATION: 1..1887
OTHER INFORMATION: any n =
NAME/KEY: misc_feature
LOCATION: 1..1887
OTHER INFORMATION: Ceres S
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                                                                                                                        TYPE: DNA ORGANISM: Zea mays subsp.
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PRIOR APPLICATION NUMBER: US 60/148,783
PRIOR FILING DATE: 1999-08-13
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CURRENT FILING DATE: 2000-08-11
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TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
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Hurban, Patrick
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Price, Jennifer
Raines, Tracy M.
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Rameaka, Joshua G.
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Slader, Ted
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Haas, William David
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               GGTACCCTTGCACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAAATGGTGCTAAT 1200
                                                                          TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG 1140
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TYPE: DNA
ORGANISM: Gossypium
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GENERAL INFORMATION:
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TITLE OF INVENTION:
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                              GAGGCATTAGATAAACTACTCTTACAAGGTCTTGATATTACGATCTTAGGTTGCAATGAC
                                                                                            GAAAATGCTATTCAATATACTATAGCAGCTGCACATGCAACATTTGACAAGAATAAGAAA
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Search completed: May 3, 2003, 21:11:50 Job time: 3833 secs
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OLASON WANTE BARGE BLANK WATER

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| 35.4 | 35.8 | 36.2 | 36.6 | 36.8 | 36.8 | 37 | 37.2 | 37.2 | 37.2 | 37.2 | 37.2 | 37.2 | 37.2 | 37.4 | 37.4 | 38 | 38 | 38 | 38 | 39 | 40.8 | 49.6 | 57.6 | 57.6 | 57.6 |
| 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.6 | 1.7 | 2.1 | 2.4 | 2.4 | 2.4 |
| 401 | 443 | 55155 | 941 | 386 | 380 | 65042 | 32249 | 32249 | 32193 | 32193 | 32190 | 32190 | 368 | 2080 | 2080 | 27681 | 27681 | 27681 | 27681 | 1523 | 486 | 2000 | 14623 | 14623 | 13917 |
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| US-09-960-352-10213 | US-09-770-444-842 | US-09-735-933-3 | US-10-123-155-464 | US-09-829-481-5 | US-09-960-352-9335 | US-10-229-124-3 | US-09-764-878-202 | US-10-079-854-202 | US-09-764-878-200 | US-10-079-854-200 | US-09-764-878-201 | US-10-079-854-201 | US-09-834-975-47 | US-09-991-936-1869 | US-09-991-936-1867 | US-09-764-869-1998 · | US-09-764-869-1997 | US-10-091-504-1998 | US-10-091-504-1997 | US-09-938-842A-4708 | US-09-878-574-4606 | US-09-938-842A-4507 | US-09-918-740-76 | US-09-918-740-74 | US-09-918-740-72 |
| Sequence 10213, A | Sequence 842, App | Sequence 3, Appli | Sequence 464, App | Sequence 5, Appli | Sequence 9335, Ap | Sequence 3, Appli | Sequence 202, App | Sequence 202; App | Sequence 200, App | Sequence 200, App | Sequence 201, App | Sequence 201, App | Sequence 47, Appl | Sequence 1869, Ap | Sequence 1867, Ap | Sequence 1998, Ap | Sequence 1997, Ap | Sequence 1998, Ap | Sequence 1997, Ap | Sequence 4708, Ap | Sequence 4606, Ap | Sequence 4507, Ap | Sequence 76, Appl | Sequence 74, Appl | Sequence 72, Appl |

ALIGNMENTS

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Best Local Similarity
Matches 2396; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Plant phosphomevalonate FILE REFERENCE: Le A 35 018 CURRENT APPLICATION NUMBER: US/09/988,863A CURRENT FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bayer AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (685)..(2199)
 241 GTTTCTCGGTTTCTTCCGAACTCCCAGGCCTAGTTTGGTTTTATTTTTTCACGAGTTTTGC
                                                                                                                                                                                                       61 AAGCAAACTGGGGAAGATGAAGATGGAGTGGTGAAGAACAAAACCGTATAACCGTTCGGT 120
                                                                                                                                                                                                                                                                              GTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACTGTCGGTTTTTTTCGGTTCGG
                                                                                                                                                TCAGAGGTGCCGAACCGAACCGGTAAACCGAAATCCTCAAAAGAAATTGCCGATCG
                                                                                                                                                                                    AAGCAAACTGGGGAAGATGAAGATGGAGTGGTGAAGAACAAAACCGTTTATAACCGTTCGGT
                                                                                                                                                                                                                                                             GTCGACCCACGCGTCCGGGCCGACCTTCTTCTTCTTCCTTAAGACAACACATAATGATAG
                                                                                                             TCAGAGGTGCCGAACCGAACCGACCCGTAAACCGAAATCCTCAAAAGAAATTGCCGATCG
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Pred. No. 0;
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| 1380 | 21 AAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTT | Ωу 13; |
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| 1320 1320 | 61 GTTGCAGCTCTGTTACATTATCTTGGAGTGGTTGACCTATCTGATCCATGTAAGAAGGA | Qy 12(рь 12(|
| 1260 1260 | 01 TCCAAGCCTGAAGTAGCAAAAACTGGCTTAGGTTCTTCTGCAGCAATGACAACAGCTGTG | Qy 120 Db 120 |
| 1200 1200 | 41 GGTACCCTTGCACCGTTTGCATCAATCACATTCAATGCTGCGGAGTCAAATGGTGCTAAT | ον 11, |
| 1140 | 81 TTTTACTCATATCGGAACCAGATAGAATCGGCTGGGCTTCCATTGACACCAGAATCGCTG | Oy 101 |
| 1080 | 21 GAATCATTGCACAAACTCTTATTGCAAGGTCTTGATATAACAATATTAGGCTCCAATGAC | Qy 10: |
| 1020 1020 | 61 GTAGAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCAACCGAGAAGGACAAA | Qy 91 Db 91 |
| 960 | 01 CTGTCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTT | Qy 91 |
| 900 | 41 TGGAAATGGACAGATGTCAAATTAACATCACCACAGCTCTCGAGAGAAAGCATGTATAAA | 8 dd 8 |
| 840 840 | 81 GCACGGTTTTACGCGATTGTGAAGCCAATCAACGAAGAAGTCAAGCCTGAAAGTTGGGCA | Qy 71 Db 71 |
| 780 780 | 21 ATGACTGGAGGCTACCTTGTACTCGAGAAGCCAAATGCAGGGCTTGTGTTTGAGTACAAAT | Qy 7: |
| 720 720 | 61 GATTATCTTTGTCACTCTTTGAAAATGGCTGTTGTTGCTTCTGCTCCTGGGAAAGTTTTG | Qy 61 Db 61 |
| 660 | 01 TCCGATCATTTCCGGCGATATCCAATCGCAGACTGAGGTGAATCTGGGGTTTTGATCAGC | Оу 61 Въ 61 |
| 600 | 41 AATCCGATCTACCACCACTACTCGTACCGCCGGTCATTTACTGCCGCCGATTTCAAATTA | ρρ 2, δλ 2, |
| 540 540 | 81 TTGAGGATCTAAATCGGAAATTGCATTAATACTCATCTCCAATCTCTTCTGAAGAGTCCG | Oy 41 |
| 480 480 | 21 CGATCCGTCTCGATCGACGGAGAGATACGTTTCGATCCGGTTTCGATCCAAATCGGAGAGT | Qy 4: |
| 420 | 61 GAGCGTCGACAGTAAGAGAAGAAGACAGCGATTGTGTGTAGATCGACGGCGAACGTGTGTT | Qy 3(|
| 360 360 | 01 TYCTCTYTTCATCGGCGACGACGACGTCGAGTTYCTGTCAAAACGTTAACGATCCGACTC | Qу 3(Db 3(|
| 300 | | Db 2, |

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| | CTTGCGGGAAAATAAAT | 2341 | Qy |
| 2340 | GCTAAATTTCTTGGTGTAAGCATTTTTATACCCCATTGTAAGGTCTTTAACTCTTG | 2281 | Db |
| 2340 | TGCTAAATTTCTTGGTGTAAGCATTTTTATACCCATTGTAAGGTCTTTAACTCTTTGGAAA 2 | 2281 | Оу |
| 2280 | CAATTATTAGGTGCGTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACTTGG | 2221 | Db |
| 2280 | CCAATTATTAGGTGCGTCACCAAGTTCGGTTGAGTATACTGTTTTGCATATAGACTTGGG 2 | 2221 | Оу |
| 2220 | CATGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTG | 2161 | рь |
| 2220 | ACATGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGT 2 | 2161 | ОУ |
| 2160 | GCCTTGTTGGTGAGAGAAGATCCACATGGCGTTTGCCTAGAAAGTGGTGATCCACGAACC | 2101 | Db |
| 2160 | CCTTGTTGGTGAGAAGATCCACATGGCGTTTGCCTAGAAAGTGGTGATCCACGAAC | 2101 | Qy |
| 0019 | ATCACTTTAGGGGATTCCGGCACCAAACTGACCCAGGCATGGAGTTCGCACAATGTTTTG | 2041 | Db |
| 2100 | ATCACTTTAGGGGATTCCGGCACCAAACTGACCCAGGCATGGAGTTCGCACAATGTTTTG 2 | 2041 | Qy |
| 2040 | GCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCA | 1981 | da |
| 2040 | GCTGAAGGAGTTCTACTTGCTGGTGTTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCA 2 | 1981 | Qy |
| 1980 | GCGGCTAGCGTTCCGATAGAGCCTGAATCTCAAACTCTTTGGATTCTACAATGAGT | 1921 | Db |
| . 0861 | GCGGCTAGCGTTCCGATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGT 1 | 1921 | Оу |
| 1920 | TCAGATGG | 1861 | дb |
| 1920 | TCTTAGAGGCAAGAAGCTATGTTGAGGATCAGAATTCTTATGCGTCAGATJGG | 1861 | Оу |
| 1860 | ACTICTGAAAAGTGGGTGTTACATGCTACTGAACCAATCAACGAAGCCATIATTAAAGAA | 1801 | Db |
| 1860 | CTTCTGAAAAGTGGGTGTTACATGCTACTGAACCAATCAACGAAGCCATTATTA | 1801 | Qy |
| 0081 | AGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTAGT | 1741 | Db |
| 0081 | AATTAGCTAAAGACCACTGGGATGTTTATCTACGAGTCATTAAGTCTTGTAGTGTGCT | 1741 | Qy |
| 1740 | AACTGGCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCTGAGC | 1681 | Db |
| 1740 | ACTGGCAGAATTTGTCAGATGCAAATTTAGAACTGGAAACTAAGCTAAACGATCI | 1681 | Qy |
| 0891 | CCATCATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAGGCACGAGAA | 1621 | Db |
| 1680 | CATCAATGGTAGGTGCAGTAAAGAAGTGGCAAATGTCTGATCCAGAGAAGGCAC | 1621 | Qy |
| 1620 | TCTTTACCACCACTGATGAATCTTTTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCACA | 1561 | Db |
| 1620 | CTTTACCACCACTGATGAATCTTTTCCTTGGAGAACCTGGAAGTGGTGGATCCTCCAC | 1561 | Qy |
| 1560 | TTAAATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAACTGAGTTC | 1501 | dd |
| 1560 | AGTT | 1501 | Qy |
| 1500 | TATGTTCGCTTCTCCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCCA | 1441 | Db |
| 1500 | ATGTTCGCTTCTCCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACAGGTCTGCC | 1441 | Qy |
| 1440 | GCACAAGGGAAGTCGGAAGTGGGTTTGATGTCAGCTGTGCTGTCTATGGAAGTCAGCGT 1 | 1381 | дд |
| 1440 | TCAC | 1381 | Qy |
| 1380 | ${\tt AAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTT} \ \ \vdots$ | 1321 | Db |

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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of I
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER CEC.
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Best Local Similarity
Matches 443; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 851
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                                                                                            CCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCACCT
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            TTGTAAGGTCTTTAACTCTTGGA 2338
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TTGTAAGGTCTTTAACTCTTGGA
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Allen, Keith
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LENGTH: 728
TYPE: DNA
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CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 5
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TITLE OF INVENTION: Plant phosphomevalonate
FILE REFERENCE: Le A 35 018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
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AGTCAGCGTTATGTTCGCTTCTCCAGAAGTCTTGTCATTTGCTCAGGTTGCAGTAACA
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                                                                                                                           ----AAGGAAAGTTTGGCTGTTCTGATCTAGATGTTATCCATATGATAGCACAAACGTCT
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                                                CACTGTATTGCCCAAGGTAAAGTTGGCAGTGGCTTTGATGTCAGTTCTGCTGTCTATGGG
                                                                                                           CACCAAGAAATAAGAATTCCACAGATCTCGATATTGTGCATATGATAGCTCAAAGTGCC
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Pred. No. 6.8
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Mismatches
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5.8e-116;
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US-09-988-863A-3
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Patent No. US20020123427A1
GENERAL INFORMATION:
APPLICANT: Bayer AG
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
ORGANISM: Medicago truncatula
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                TTAGGTTCTTCTGCAGCAATGACAACAG 1255
                                                                                      ACATTCAATGCTGCGGAGTCAAATGGTGCTAATTCCAAGCCTGAAGTAGCAAAAACTGGC 1227
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                                                                  TCTTTCAATACTGATGATGCTAATGGAAGGAATTGTAAGCCTGAAATTGCCAAAACTGGT
                                                                                                                                        AGACACGGACTCCCTTTGACATCAGAATCATTGGCCACCCTTCCGCCTTTTGCCTCCATT 523
                                                                                                                                                                         TCGGCTGGGCTTCCATTGACACCAGAATCGCTGGGTACCCTTGCACCGTTTGCATCAATC 116;
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Pred. No. 2.2e-78;
0; Mismatches 158;
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RESULT 5 US-09-909-745-21

Sequence

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Application US/09909745

RESULT 6
US-09-909-745-19
; Sequence 19; Application C; Patent No. US20020119546A1

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GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
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SEQ ID NO 21
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TYPE: DNA
ORGANISM: Oryza
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CURRENT FILLING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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PRIOR FILING DATE: 1998-11-05
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                                  AA 2202
                                                                                                        AAAGTGGTGATCCACGAACCACATGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGT
                                                                                                                                              GGAGCTCAGCTGGTTCTCCCCTCTTCTTGTTCGAGAAGATCCCCGAGGTGTTTCATTGG
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                                                                      AAGCTGGTGACCCAAGAACAAGGGAGGTGTCAACCGCTGTATCATCGATACAAATAAACT
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SEQ ID NO 19
LENGTH: 539
TYPE: DNA
ORGANISM: Oryza sativa
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Best Local S
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
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PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                              1721
2020 GGATT 2024
                                                                                                                                                                        1841 ACGAAGCCATTATTAAAGAACTCTTAGAGGCAAGAGAAGCTATGTTGAGGATCAGAATTC
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OCATION: (287)
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                                                     CTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTACTTGCTGGTGTTCCTGGAGCTGGT 2019
                                                                                     ATATGCCAAGAGATGGGCATAGCAGCTGGTTCCAATTGAGCCAGAATCACAAACTCAA
                                                                                                                                             AAGAACTAATTGTTAGATCATTACTGGCCGCAAGAGATGCTTTCCNTGAAATAAGGCTTC
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(465)
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US-09-887-576-273/c
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CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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APPLICANT: Bayer AG
TITLE OF INVENTION: Plant phosphomevalonate kinases
FILE REFERENCE: Le A 35 018
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                APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
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TYPE: DNA
ORGANISM: Pinus radiata
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APPLICATION NUMBER: US 60/258,692
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Han, B.
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US-09-909-745-15
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; ORGANISM: Arabidopsis thaliana
US-09-887-576-273
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Best Local Similarity
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909/745
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Office 97
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SOFTWARE:
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                                                                      1909 CAGATGGGTGAGGCGGCTAGCGTTCCGATAGAGCCTGAATCTCAAACTCAACTTTTGGAT 1968
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                                                                                                                                                                                    249 TGTAGTCGTCTCACATATGGGAAGTGGGCAGAGGTGGCTACTAACCAACATCAAGAATTA 190
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                                      GAGATGGGCATAGCAGCTGGTGTTCCAATTGAGCCAGATTCACAAACACGGCTACTAGAT
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US-09-909-745-17
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                                                                                                                                                                                                                                                                                                                      RESULT 11
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Best Local Similarity
Matches 160; Conserv
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FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
                                                                                                                    APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                              APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/90: CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
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TYPE: DNA
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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                                                                                                                                                                                                                                                                               Application
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Pred. No. 1.7e-21;
0; Mismatches 88;
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-204
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Best Local Similarity
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TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
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PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
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                 GTTTTTTCGGTTCGGGTTTCTCCGGTTTCCTTCCGAACTCCCAGGCCTA 272
                                                                        TAATTTGGCCGATCGGTTCGATCTCCTTAATTCGGTTGCTGCCGAAAACCAAAATTTTCG 1374
                                                                                                         AGAAATTGCCGATCGGTTTGCTACTGTTCAAAACCTCGGTGCCGAGAACCGAAACTGTCG 225
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TTTTTTCGGTTCGGTTTCTCGGGTTGAACCGTTATCCCAGGCCTA 1421
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Chang, H.
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70.1%;
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Pred. No. 5.3e-15;
0; Mismatches 56;
                                                                                                                                                                                                                                         Score 76.6; DB 10
Pred. No. 9.3e-12;
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                             DB 10;
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; TYPE: DNA
; ORGANIZM: Saccharomyces cerevisiae
US-09-918-740-48
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Best Local Similarity
Matches 138; Conserv
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LENGTH: 1356
                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEC. TO THE STATE OF SEC. TO THE SEC. TO THE STATE OF SEC. TO THE SEC. 
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APPLICANT: Kuehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid
TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
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TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathway
TITLE OF INVENTION: create novel traits in transgenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/918,740 CURRENT FILING DATE: 2001-07-31
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                                                                                                                                               LENGTH: 7681
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Operon C containing A. tha OTHER INFORMATION: CL190
OTHER INFORMATION: DNA, and R. capsulatus DNA
                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1337 ATCTAGATGTTATCCATATGATAGCACAAACGTCTCATTGTCTTGCACAAGGGAAGGTCG. 1396
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Pred. No. 3
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3.2e-06;
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; ORANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Operon containing A. thaliana and S. cerevisiae DNA
US-09-918-740-58
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Best Local Similarity 50.7%;
Matches 138; Conservative
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Best Local Similarity
Matches 138; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 58 LENGTH: 7693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/09/918,740
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
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APPLICANT: Kuehr
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ITLE OF INVENTION: Kraipulation of genes of the mevalonate and isoprenoid pathways
ITLE OF INVENTION: create novel traits in transgenic organisms
4578 TAACTTTATGGATGGGCGATATTAAGAATGGT 4609
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                                                                                            ATTTGGTTGATGAAGAAGACTGGAATATTACGATTAAAAGTAACCATTTACCTTCGGGAT 4577
                                                                                                                                                                                         CCGCATTAATCTCTAATTTGCCAGATATTGGAAGTGCTACTTACGGCAGTAAACTGGCGC
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Pred. No. 1.1e-05;
0; Mismatches 134; Indels
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US-08-232-463-14/c
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                            TYPE: n
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                                                       STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                               FILING DATE: APPLICATION NUMBER: FILING DATE: 26-AUG
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                                                                                                                        TELEX: 899149
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US-09-590-101A-9
US-09-590-101A-9
US-08-232-463-14
US-09-356-952-9
US-09-134-001C-1073
US-08-265-087-3
US-08-265-087-3
US-08-265-688-3
US-08-265-688-3
US-09-345-882-1
US-08-245-09-3
US-08-245-09-3
US-08-245-09-3
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Minimum Maximum

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441362 seqs, 153338381 residues

Scoring table: Sequence: Title: Perfect score:

IDENTITY_NUC Gapop 10.0 ,

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US-09-988-863A-1 2396

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

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Issued_Patents_NA:*

654321

/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Result

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7218 65042 18627 168575 169998

-09-784-316-3

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US-09-426-290-1
US-09-676-610B-24
US-09-525-232-5
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US-08-544-332-25
US-08-107-755A-1
US-08-107-755A-1
US-08-544-332-1
US-08-544-332-1
US-09-370-861A-1
US-09-370-861A-1
US-09-370-861A-1
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US-09-370-861A-1
US-09-370-861A-1
US-09-370-861A-1
US-09-370-861A-1
US-09-384-32-28
US-09-384-32-28
US-09-384-8
US-08-990-571-8
US-09-134-001C-277
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US-09-134-001C-2187
US-09-357-251-25

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Query Match

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1494 TCTGCCATTAAATGAAGTTATTGGTACAATTTTGAAGGGAAAATGGGACAATAAGAGAAC 1553

Best Local

Similarity 23; Conserv

Conservative

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Pred. No. 0.0038; l3; Mismatches 177;

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; LOCATION: (1)...(65042)
; OTHER INFORMATION: n = .
US-09-784-316-3
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US-09-784-316-3
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Patent No. 6461843
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/784,316
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ACITITLE OF INVENTION: THE FILE REFERENCE: CL001139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WEI, Ming-Hui et al. TITLE OF INVENTION: ISOLATED HU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
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                                                                                                                                 44535
                                                                44595
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                2284
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                                                                                                                                                2164 TGTATTACTTCAGGCGTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGTCCA 2223
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                              TAAATTTCTTGGTGTAAGCATTTTTATAC 2312
                                                                                                                              TTTTTTCATTCTATTTTCTCTGTTATTCAGATTGGGTAATTTACATTGTTCTATTTTCCA 44594
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                                                               GTTCATTGATTATTTCCTCTGTCCCCTGCATTCTGTTGTTGAGCCTATCTACTGAGCTTT 44654
                                                                                               ATTATTAGGTGCGTCACCAAGTTCGGTTGAGTATACTGTTTTTGCATATAGACTTGGGTGC 2283
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SOFTWARE: SEQ ID NO 1

FastSEQ for Windows Version 4.0

ORGANISM: Homo Sapiens FEATURE:

TYPE: DNA

LENGTH: 168575

CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 24

US/09/426,290

GENERAL INFORMATION:

APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN WARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000

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US-08-961-527-113
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Best Local Similarity
Matches 61; Conserv
Sequence 1, Application US/09426290 Patent No. 6410712
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                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                  15547 GTGCCACCACTTGCAATCTTTGTCGCAACTCTTCTTTTCAAAGA 15590
                                                                                                                                                                   15487 GCAGCAACTGTTTCTTCAGGTGGTTCTGTAGCCATGGCAGCAGTTATGGCTGGAGGAATG 15546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                  1273 TTACATTATCTTGGAGTGGTTGACCTATCTGATCCATGTAAAGA 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: doub
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Pred. No. 5.6;
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RESULT 5
US-09-676-610B-24
; Sequence 24, Application US/09676610B
- Datent NO. 6444465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION FILE REFERENCE: RTS-0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 169998
TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 21;
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                              AGAGCATGCGATACAGTATGCTATAGCTGCTGCTCATTTGGCAACCGAG 1011
                                                             TCAGATAATTAAGACAATTCATTCTCCTGAAACTGCTGTTCATGTAAAAAGGAATTTTAT
                                                                                                                           GAAATTCACTAAATGCAAATAAACCTAGCAAATGCTCTATGGTTAATTTTTTTCTAAAAT 51300
                                                                                          GTCACTGAATCATTTGACTCTTCAGTCTGTGTCTGCAAGTGATTCAAGAAACCCCTTTGT
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Score 34.6; D Pred. No. 33; O; Mismatches

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; OTHER INFORMATION: WHerein any n is a, g, c, US-09-552-322-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-07-991-867B-25/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/07991867B Patent No. 5476781
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/552,322 CURRENT FILING DATE: 2000-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gould-Rothberg APPLICANT: Rastelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/193,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 15966-548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING OF INVENTION: DIFFERENTIAL GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Assembled OTHER INFORMATION: using sequences from AC024267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION:
              CLASSIFICATION: 435
RIOR APPLICATION DATA:
                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      FILING DATE:
                                                                    APPLICATION NUMBER:
                                                                                                                                                        MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                       ADDRESSEE:
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NO. 6436642
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                                                                                     APPLICATION DATA:
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                                                                                                                                                                                                                                                                     E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                            Gruidl, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Moyer, Richard W.
                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                          Floppy disk
                                                    12-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                               Richard L.
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WO 92/14818
                                                                   US/07/991,867E
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Pred. No. 2.5;
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US-08-107-755A-25/c
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                                APPLICATION NUMBER: US 0 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
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                                                                                                    APPLICATION NUMBER: US 0:
FILING DATE: 30-JAN-1992
                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 19-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TOPOLOGY: unl
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REFERENCE/DOCKET NUMBER: UF114.C3
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Local Similarity 56.8%;
es 63; Conservat:...
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   REGISTRATION NUMBER:
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                  Saliwanchik, David R
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                                                                                                                                                                                                                                                                                                                                                       Florida
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                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                         David R. Saliwanchik
                                                                                                                                                                                                                                                                                Floppy disk
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31,794
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TELEPHONE:

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GENERAL INFORMATION:
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APPLICANT:
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           TELEPHONE: 904-375-8100
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO 92/14818
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                            FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 ATAAAATCTAAATTTGAATTTAAAAAAATTATTATTCTATGAGTTTTATTGGTGATTTA 232
                                            NAME: Bencen, Gerard H. REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                               FILING DATE:
                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 1.4%;
Local Similarity 56.8%;
                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICANT: Hall, Richard L.
LICANT: Gruidl, Michael E.
LE OF INVENTION: No. 5935777el Entomopoxvirus Expression
BER OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĘĽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08544332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Gerard H. Bencen
2421 N.W. 41st Street, Suite A-1
904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moyer, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                             12-FEB-1992
                                                 NFORMAL, Gerard H. 35,746
                                                                                                                                                           30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372-5800
                                                                                                                            US 07/657,584
                                                                                                                                                                            US 07/827,685
                                                                                                                                                                                                                                                                            US 08/107,755
                                                                                                                                                                                                                                                                                                                              US 07/991,867
                                                                                                                                                                                                                                                                                                                                                                                             US/08/544,332
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                                              UF114.C4
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                                                                                                     RESULT 11
US-08-107-755A-1/c
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                              Sequence 1, Application US/08107755A Patent No. 5721352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E. APPLICANT: Grand M. Additional Control of the Control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1992-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/107,755 PRIOR FILING DATE: 1993-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: UF114.C4.D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1395
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1936 ATAGAGCCTGAATCTCAAACTTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
                                                                                                                                                                                                                                                                                                 1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
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LENGTH: 1395 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1936 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: un MOLECULE TYPE:
                                                                                                                                                                                                                                                       231 TTGGCTAGTAGTAGAGGTGCATTATTTATTTCTAGATATGATATTAAT 181
                                                                                                                                                                                                                                                                                                                                                                                                  291 ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 232
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mes 63; Conserv
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les 63; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/657,584
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34.2; D
Pred. No. 2.3;
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Pred. No. 2
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APPLICANT: APPLICANT: APPLICANT:

Moyer, Richard W. Hall, Richard L. Gruidl, Michael E.

TITLE OF INVENTION:

No. 5721352el Entomopoxvirus Expression System

NUMBER OF SEQUENCES:

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                                                                                                                                                                              ; LOCATION:
US-08-107-755A-1
                                                                                                                      Matches
                                                                                                                                   Query Match
Best Local Similarity
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                  1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
                                                                                     1936 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
                                                           355
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 6768 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
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PRIOR APPLICATION DATA:
07/827,658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLECULE TYPE:
295 TTGGCTAGTAGTATAGAGGTGCATTATTTATTTCTAGATATGATATTAAT 245
                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                         ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (904)
                                                                                                                     Conservative
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3080..6091
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1474..2151
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2502..2987
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 6.1;
                                                                                                                     Mismatches
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                                                                                                                                              DB 1;
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                                                                                                                                               Length 6768;
                                                                                                                   Indels
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RESULT 12

Conservative

0;

Mismatches

48;

Indels

0

Gaps

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us-07-991-867B-1
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Best Local Similarity Matches 63; Conserv
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                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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LENGTH: 8457 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NERAL INFORMATION: AppLICANT: MOTER, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
APPLICANT: Gruidl, Michael E.
TYPE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
                                                                                                         FEATURE
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5. 5476781
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2502.
                                                                         CDS complement (6277..6768)
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3080..6091
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PC-DOS/MS-DOS
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                1.4%;
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                Score 34.2;
Pred. No. 7;
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                               DB 1;
                              Length 8457;
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1936 ATAGAGCCTGAATCTCAAACTTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995

ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 296

FEATURE:

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US-08-544-332-1/c
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                                                                                                                                                                                                                TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA:
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                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
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                    EATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                 NAME/KEY:
                                                                                 ORGANISM:
                                                                                                                                    TOPOLOGY:
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NAME/KEY:
                                  LOCATION:
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                                                CDS
                                complement (65..1459)
                                                                                 Amsacta moorei entomopoxvirus
                                                                                                                                 unknown
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                                                                                                                 DNA (genomic)
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19-FEB-1991
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US-09-370-861A-1/c
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                                                                                                                        Query Match
Best Local S
Matches 63
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1992-02-12 PRIOR APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/370,861A
                                                                                                                                                                                            LENGTH: 8457
TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
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                                                                                                                                                                                                                                                                                    NUMBER OF
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                                                                                         1936 ATAGAGCCTGAATCTCAAACTCAACTTTTGGATTCTACAATGAGTGCTGAAGGAGTTCTA 1995
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                            1996 CTTGCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACT 2046
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295
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                                                           355 ATAAAATCTAAATTTGAATTTAAAAAATTATATTATTCTATGAGTTTTATTGGTGATTTA 296
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                                                                                                                          Local Similarity
nes 63; Conserv
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TTGGCTAGTAGTTATAGAGGTGCATTATTTATTTCTAGATATGATATTAAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                                     8457
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                                                                                                                                                                                                                                                                   PatentIn version 3.1
                                                                                                                                                                                                                                                                                    SEQ ID NOS:
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2502..2987
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Pred. No. 7;
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RESULT 15 US-09-253-316-3/c ; Sequence 3, Application US/09253316

Patent No. 6395890 GENERAL INFORMATION:

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Search completed: May 3, 2003, 20:11:34 Job time: 1035 secs
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; LOCATION: (1)...(1062)
; OTHER INFORMATION: n = A,T,C or G
US-09-253-316-3
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Best Local Similarity 28.8
watches 78; Conservative
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1062
TYPE: DNA
ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: US 60/075,300
EARLIER FILING DATE: 1998-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Degenerate sequence
FEATURE:
                                                                                                                                                                                                          2179 GTTTCATCAATTCACCTTGAGTAAACAACATTGTTTCAGTGTCCAATTATTAGGTGCGTC 2238
                                                                                                                                                                                                                                                                                              2119 GATCCACATGGCGTTTGCCTAGAAAGTGGTGATCCACGAACCACATGTATTACTTCAGGC 2178
                                                                                                                                                                                                                                                                                                                                                                 1999 GCTGGTGTTCCTGGAGCTGGTGGATTTGATGCCATATTTGCAATCACTTTAGGGGATTCC 2058
                                                                                                                         2239 ACCAAGTTCGGTTGAGTATACTGTTTTGCAT 2269
                                                                                 591 NGCNGGCATNGTYTTRTANSWNGTNSWNARY 561
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                                                                                                                                                                                                                                                       RTTNSWRTTYTCRTTNGTNACNCKRTTNSWDATNCCCATNCCRCANGTNCKNSWRCANGG 652
                                                                                                                                                                    NGTCCAYTINGINGCYIGNACNARRCAYTIYTIYTICCADAINARNGGNARRIINCKRIA 592
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28.8%;
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length: 2000000000
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O9fd67 enterococu
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09ut88 schizosacch
0973b5 sulfolobus
097ul6 sulfolobus
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| 106 | 106 | 106 | 106.5 | 107 | 108.5 | 108.5 | 108.5 | 109 | 109.5 | 109.5 | 110.5 | 112 | 112.5 | 112.5 | 114 | 114 | 115 | 115.5 | 117 | 117.5 | 118.5 | 123.5 | 124.5 | 125 | . 125 | 126.5 | 130 | 130.5 |
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| 4.1 | 4.1 | 4.1 | 4.1 | 4.1 | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 | 4.3 | 4.3 | 4.4 | 4.4 | 4.4 | 4.4 | 5 | 4.5 | 4.5 | 4.6 | 4.6 | 4.8 | 4.8 | 4.8 | 4.8 | 4.9 | 5. O | 5.1 |
| 1087 | 667 | 382 | 715 | 463 | 1477 | 659 | 615 | 3475 | 1348 | 1101 | 1417 | 797 | 902 | 478 | 3919 | 823 | 816 | 4625 | 386 | 721 | 334 | 352 | 317 | 816 | 376 | 241 | 816 | 434 |
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| 082303 | Q67482 | Q94BU9 | 030965 | Q9S243 | Q48028 | Q8ZHG8 | Q8UAJ0 | Q9U175 | 008828 | Q9NXY9 | Q9HWR8 | Q8TPP4 | Q91742 | Q8UHF9 | Q9СРН9 | Q9VWB0 | Q9CHS9 | Q9SMH3 | Q944G2 | Q8YM05 | Q8U0F3 | Q8SUB3 | 051630 | Q9ZIL9 | Q9STB1 | Q9D0B4 | 062219 | Q9D307 |
| O82303 arabidopsis | Q67482 japanese en | Q94bu9 arabidopsis | O30965 rhizobium l | Q9s243 streptomyce | Q48028 haemophilus | Q8zhg8 yersinia pe | Q8uaj0 agrobacteri | Q9u175 leishmania | 008828 mus musculu | Q9nxy9 homo sapien | Q9hwr8 pseudomonas | . Q8tpp4 methanosarc | Q9i742 pseudomonas | | Q9cph9 pasteurella | a. | | Q9smh3 chlamydomon | Q944g2 hevea brasi | Q8ym05 anabaena sp | Q8u0f3 pyrococcus | Q8sub3 encephalito | 051630 borrelia bu | Q9zil9 lactococcus | | Q9d0b4 mus musculu | 062219 caenorhabdi | Q9d307 mus musculu |

ALIGNMENTS

| DR | DR | RL | RT | RT | RA | RA | RA | · · · RA | RA | RA | RA | RA | RA | RA | RA | RA | RA | RA | RA | RA | RX | RC | RP | RN | ox X | გ | 8 | 8 | SO | GN | DE | DT | DT | DT | AC | ID | Q9C6T1 | DEC! |
|--|-----------------------------|---------------------------|-------------|---|---------------------------------|---|--|----------|---|---|--|---|--|----|--|--|---|-------|------------------------|--|------------------------------------|----------------------|--------------------|---|------------------|--|---|--|---|----|-------------------|---------------------------------|-------------|--------------------------------------|---------|----------------------------------|--------|--------|
| TIGRFAMS; TIGR01219; Pmev_kin_ERG8; 1. | EMBL; AC079041; AAG50716.1; | Nature 408:816-820(2000). | thaliana:"; | "Sequence and analysis of chromosome 1 of the plant Arabidopsis | Fraser C.M., Venter J.C., Davis | Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., | Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., | Š | Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., | randa M., Nguyen M., Nierman W.C., Osborn | Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., | Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li YP., | Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., | - | Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., | u P., Feldblyum T.V., Feng JD., Fong B., Fujii C.Y., | Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., | C.W., | jo R., Bowman C.L., Br | Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., | MEDLINE=21016719; PubMed=11130712; | STRAIN=CV. COLUMBIA; | SEQUENCE FROM N.A. | (1) · · · · · · · · · · · · · · · · · · · | NCBI_TaxID=3702; | eurosids II; Brassicales; Brassicaceae; Arabidopsis. | æ | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | Arabidopsis thaliana (Mouse-ear cress). | | l 54.4 kDa protei | (TrEMBLrel. 21, Last annotation | (TrEMBLrel. | 01-JUN-2001 (TrEMBLrel. 17, Created) | Q9C6T1; | Q9C6T1 PRELIMINARY; PRT; 505 AA. | 571 | TT - 1 |

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Best Local
                                                                STRAIN-CV. RRIM600; Hallahan D.L., Keiper-Hrynko N.M.; Hallahan D.L., Keiper-Hrynko N.M.; "Genes involved in the biosynthesis of isopentenyl diphosphate rubber tree Hevea brasiliensis."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF429385; AAL18926.1; -.
                                                                                                                                           Hevea brasiliensis (Para rubber tree).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids I; Malpighiales; Euphorbiaceae; Hevea.
                                                                                                                                                                                                                       Q944G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein SEQUENCE 505 AA; 5
                                                       TIGRFAMs;
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01-JUN-2002
                                        SEQUENCE
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                             Phosphomevalonate kinase.
Local . 374;
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              Similarity
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                                                         TIGR01219;
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(TrEMBLrel. 21, Last annotation update)
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              74.8%;
74.1%;
                                                        Pmev_kin_ERG8;
     Score 1930.5; DB 1
Pred. No. 2.7e-140;
51; Mismatches 67;
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Pred. No. 1
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                                        BE6F91B80B45FF94
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     KSPQFINAEWLYNIDWTVSPIRVHQIYENCELEKNPNPFVQLALFYVI-NYFFSTGR---
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Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B. Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AL109739; CAB52264.1; -TIGRFAMS; TIGR01219; Pmev_kin_ERG8; 1.
                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative phosphomevalonate kinase.
SPAC343.01C.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4896
                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                    MAVVASAPGKYLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL
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TSPQ-LSRESMYKLSLN------HLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKE
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                                  MKVTCSAPGKVLIAGGYIVLDPQYSGLVIGLTAKGYASTTTLDD
                                                                                                                      Similarity
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                                                                                                     Conservative
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                                                                                                                    Score 493; DB 3; Pred. No. 1.3e-29;
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                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7."; DNA Res. 8:123-140(2001).
EMBL; AP000984; BAB65998.1;
                                                                                                                                                                                                                                                                                                                                                                                                              Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y. Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi & Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshina T., Kikuchi H.;
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                                                                                                                                                                                                                                                    Hypothetical prote SEQUENCE 314 AA;
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PubMed=11572479;
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01-JUN-2002
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                                                                                                                                                                                                                                                                                         Pfam; PF00288; GHMP_kinases;
                                                                                                                                                                                                                                                                                                               InterPro; IPR001745; GHMPknse_ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                       SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAI - - VKPINEEVKPESWAWKWTDVKLTSP
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                                                                                      SAPGKILWIGSYSVV
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1 (TrEMBLrel. 19, 1
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al protein ST0978.
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                                                                                                                                                                                                                                                    protein; Complete proteome.
l4 AA; 35307 MW; 89740213AB16335F CRC64;
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23.2%;
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                                                                                                                                                                    64;
                                                                                                                                                                Score 235; DB
Pred. No. 6.3e
64; Mismatches
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                                                                                    FGGISHVIAINKRVR
                                                                                                                                                                                       235; DB 17;
No. 6.3e-10;
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Best Local
                                                                                                                                                                                                                                                                         "The complete genome of the crenarchaeon Sulfolobus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001). InterPro; IPR001174.
                                                                                                                                                                                                          PRINTS;
Kinase;
                                                                                                                                                                                                                                                                                                                                                       She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Per Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup Charlebois R.L., Doolittle W.F., Duguet M., Gaasteland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPR001745; GMPKnse_ATP.
Pfam; PF002288; GMmP kinases; 1.
PRINTS; PR00960; LMBPPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus solfataricus.
Archaea; Crenarchaeota;
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 TSPQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119
                                                          -EGLRIEA 314
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                                       IKVSAPGKILWIGSYSVV---FGGISHVIAVNKRVSCSLREIKE-----
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                                                                                                                                Similarity
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                                                                                                                                8.9%;
22.2%;
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                                                                                                             72;
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Last annotation updat
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                                                                                                                              Score 230; DB 17;
Pred. No. 1.6e-09;
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                                                                                                                                                                                       D62E48552F5CBDF8 CRC64;
                                                                                                               Mismatches
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                                                                                                                                                  Length
                                                                                                               Indels
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01-MAR-2001
01-JUN-2002
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EMBL; AF290093; AA602442.1; ---
Interpret Transparence.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001745; GHMPknse_ATP.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20353468; PubMed-10894743;
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NCBI_TaxID=1351;
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                                                      PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
                                                                                                               IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIDVKED-EGLRLES 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVL 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGS
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                                                                                                                                                                                                                                     106;
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 PR00959; MEVGALKINASE.
s; TIGR01220; Pmev_kin_
                                                                                                                                                                                                                                                                                                                                                        368 AA; 40541 MW; 390993D36577146D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AEEEGALVALSPGAGGGDSIFA--LGNDLNRVREAWSKRGIF 308
                                                                                                                                                                                                                                                                                                                                                                                                           Pmev_kin_Gr_pos; 1.
                                                                                                                                                                                                                            6.9%; Score 178.5; DB 2; 22.3%; Pred. No. 1.8e-05; Live 58; Mismatches 179;
----ENPF-----HYVLAAIHL-TEKYAQEQNKEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                  Indels 133;
                                                                                                                                                                                                                                                                                        Length 368;
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| LAL 4 | 16 VPIEPESOTOLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGT-KLTQAWSSHNV | ο _ν ξ | |
|----------------------------|--|--------------------------|---|
| AAS 41 INO 22 | WVLHATEPINEAIIKELLEAREAMLKIRILMKQMGE | γ., g | : |
| 18 | 48 DMKLMIGWSQKPASTSRLVDETNANKAALNTEYK | Db | |
| KLA 355 | 298 -MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKAR-ENWQNLSDANLELETKLNDLS | Qy | |
| .PPL 297 РРН 147 | 239 SGFDVSCAVYGS-QRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLP ::: ::: :: ::: 5 SAGDIAASVYGGWLAYQTFDKKWLQY-ELANKTLSDVVNEAWPGLKIELLTP | Db. | |
| KVG 238 | 179 KTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKBGKFGCSDLDVIHMIAQTSHCLAQGKV | Оу | |
| Gaps | ery Match 6.1%; Score 158.5; DB 2; Length 294; st Local Similarity 24.8%; Pred. No. 0.00045; tches 75; Conservative 42; Mismatches 117; Indels 69; | Que Bes Mat | |
| | 01220; Pmev_kir AA; 32537 MW; | SQ SQ | |
| | <pre>MBL; AJ279018; CAC51372.1; nterPro; IPR001745; GHMPknse_ATP. fam; PF00288; GHMP_kinases; 1.</pre> | | |
| Þ | | | |
| | NCE FROM N N=53/7; | R R R R | |
| les; | <pre>bbacillus helveticus. eria; Firmicutes; Bacillus/Clostridium group; Lactobacilla bbacillaceae; LactobacillusTaxID=1587;</pre> | 288888 | |
| | 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Phosphomevalonate kinase. | | |
| | LT 7 31 Q93K31 PRELIMINARY; PRT; 294 AA. Q93K31; | RESULT Q93K31 ID Q | |
| 348 | 95 TEALKNLCDLAESYTGAAKSSGAGGGDCGIVIFRQKSGILPLMTAWEKDGITPL | . 문 | |
| 74 | TKLTOAWSSHNV | 9 5 | |
| PIE 419 | 60 DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIR | P 09 | |
| 264 | | Db | |
| DHW 359 | PSMVGAVKKWQMSDPEKAR | VΩ | |
| PLMN 299 : PKQLR 215 | 241 FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT-EFSLPPLMN : : | ОУ | |
| GSG 240 GSC 161 | 183 GSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG | Оy | |
| RKYGL 117 | 97SFYHLKRK | Db | |
| TGL 182 | 123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL | Qy | |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR001745; GHMPknse_ATP.
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EMBL; AB037666; BAB07792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20353446; PubMed=10894721;
Takagi M., Kuzuyama T., Takahashi S.,
"A gene cluster for the mevalonate pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Actinomycetales; Streptomycineae; Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces sp. (strain CL190).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFR 286
LMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVP-GAGGFDAIFAITLGDSGTKLT-
: : | | | | | | | | | | | | | | | : : : |
                                                                                                                                                                         EFSLPPLMNLFL----GEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELE
                                                                                                                                                                                                                                                                 CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWKWTDVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVRHAPGKLFVAGEYAVVDPGNPAILVAVDRHISVTVSDADADTGAADVVISSDLGPQAV 67
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                                                                                                    TKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRI
                                                                                                                                               R-RLPAPKGLTLEVGWTGEP
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97; Conserv
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                                                                                                                                                                                                                            -PKGSGGDLAASTWGG--WIAYQAPDRAF----VLDLARRVGVDRTLKAPWPGHSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR01220; Pmev_kin_Gr_pos; 1.
>S00141; ASP_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                           -RKFGLGSSGAVTVATVAAVAAFCGLELSTDERFRLAMLATAELD------
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                                                                                                                                                                                                                                                                                                                                                                                             -SAIETVGRLLGERGQKVPALTLSVSSRLHEDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 172;
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pathway
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01-DEC-2001
01-JUN-2002
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget Dentian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nordsiek G., Novella S., de Pablos B., Perez-
Remmel B., Rose M., Schlueter T., Simoes N.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cc
"Comparative genomics of Listeria species.";
Science 294,849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; B
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=CLIP 11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMs; TIGR01220; Pmev_kin_Gr_pos;
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InterPro; IPR001745; GHMPknse_ATP.
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                       MLQIETLEEPVPTFSVGWTGT-PVSTGKLVSQIHAFKQED---
                                                           NKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNI,SDANLELET
                                                                                                                                             QTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWD
                                                                                                                                                                                                                          NGANSKPEVAKTGLGSSAAMTTAVVAALL~-HYLGVVDLSDPCKEGKFGCSDLDVIHMIA 226
                                                                                                                                                                                                                                                                                                                                                      DGEHWTFT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PGKLYVAGEYAVVESGHTAILTAVN-RYITLTLEDSERNELWIPHYENPVSWPIGGELKP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVK----
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360 AA; 40110 MW; OFFDD7B062B42584 CRC64;
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MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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SEQUENCE 3
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TIGRFAMs; TIGR01220; Pmev_kin_C
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EMBL; AL591973; CAC98227.1; -.
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Remmel B., Rose M.,
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                                                                                                       112 SG-----KYGLGSSAAATVAVINALMTKFYPEISMLK-----KF------KLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlueter T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%;
20.5%;
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9981 MW; 15156C40BD997A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchrieser C., Rusniok C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 149.5;
                                                                                                                                                                                                                                                    ----TFLKSEGIELTPVKM-----IIETELIDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amend A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Purcell R.
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| | 243 VSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL 297 | γ |
|-----|--|----------|
| | 118 GSSGAVTVATVKALNVFYALNLSQLEIFKIAALANLAVQDNGSCGD 163 | B |
| | SSAAMTTAVVAALLHYLGVVDLSDPCKEGKF | γ |
| | 97SFYDLKRKYGL 117 | g |
| | 123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL 182 | ¥ |
| | 63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122 | ₽ 2 |
| | 60 | b |
| | 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62 | Σy |
| 19; | Ouery Match 5.7%; Score 147.5; DB 2; Length 361; Best Local Similarity 21.2%; Pred. No. 0.0044; Matches 102; Conservative 64; Mismatches 171; Indels 145; Gaps | Qu Ma |
| | SEQUENCE 361 AA; 39573 MW; 78D2796FC68A0B81 CRC64; | |
| | TIGRFAMS; TIGR01220; Pmev_kin_Gr_pos; 1. PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1. | 2 2 2 |
| | Pfam; PF00288; GHMP_kinases; 1. PRINTS; PR00959; MEVGALKINASE. | S S |
| | InterPro; IPR001745; GHMPknse Arp. InterPro; IPR001459; Mev_gal_kin. | ¥ ¥ |
| | EMBL; AF290095; AAG02447.1; Interpro; IPR000515; BPD transp. | ¥ ¥ 8 |
| | s in gram-positive cocci. | 2 2 2 |
| | Brown J.K., Bryant A.F., Chalker A.F., Holmm, Iordanescu S., So C.Y., Rosenberg M., Gwylni De evolution and essentiality of the mevalun | 3 8 8 |
| | | 2 2 |
| | NCBI_TaxID=1352; | 2 2 2 |
| | Enterococcus faecium (Streptococcus faecium). Bacteria; Firmioutes; Bacillus/Clostridium group; Lactobacillales; | 828 |
| | | SNE |
| | (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. | 444 |
| • | | 5 U 2 |
| | SULT 11 | RESU |
| | 339 EW 340 | 9 |
| | 465 AW 466 | γ |
| | 286GTKAGVNIETSLLKELADSAENMGGAGKSSGSGGDCGIAFSKTKELAEKLVN 338 | B 7 |
| | ************************************** | |
| | 347 KLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRIL 406 318 NETUK | ₹ ¥ |
| | 203 MLQIETLEEPVPTFSVGWTGT-PVSTGKLVSQIHAFKQEDSKNYQHFLT 250 | b |
| | 287 NKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELET 346 | Ωy |
| | 150 ALSHLVVQGNGSCGDIASCMYGGWIAYTTFDQEWVKH-RLAYKSLEWFMKEPWP 202 | В |

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Q9FD72
ID Q9FD7
AC Q9FD7
AC Q9FD7
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D7 01-MA
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Best Local
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BMBL; AF290091; AA602437.1; -
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InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
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01-JUN-2002
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01-MAR-2001
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MEDLINE=20353468; PubMed=10894743;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                   DVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMN 299
DIAVSVYSGWLAYSTFDHDWVK-QQMEETS----
                                                                                                                                                                                                            -----TIDSNLADNSG------QKYG
                                                                                                                                                                                                                                                                GLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTG
                                                                                                                                                                                                                                                                                                                        KTLHYEPVKFDRNEDRIEISDVQAAKQ-----LKYVVTAIEV----
                                                                                                                                                                                                                                                                                                                                                                    PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                           IQVKAPGKLYIAGEYAVTEPGYKSILIAVNRFVTATIEASNK-----VEGSIHS
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                                                                                                        LGSSAAVLVSVVKALNEFYG
                                                                                                                                                       LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGF 241
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(TremBLrel 16, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 142.5;
19.8%; Pred. No. 0.0
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2; Mismatches 1
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-- VNDVLEKNWPGLHIEPLQAPENME
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                                                                                                      YIYKLAVIANMKLQSLSSCG-
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| | SEKWVLHATEPINEATIKELLEAREAMLRIRILMROMGEAASVP 417 | 58 HWDVYLRVIKSCSVLTS : : | у 35 | Qγ |
|-----|--|---|------------------------------|-------------|
| | PHEVSEVERLE SDP | GWTGSPASS- | N) | 뫄 |
| | MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKD 357 | 298 MNLFLGEPGSGGSST | | Qγ |
| | RFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPL 297 | 40 GFDVSCAVY-GSQRYVRFSPEVLSFA : : | 1 2 | Db 04 |
| | VVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGS 239 : : : : : | 0 TGLGSSAAMTTA : : 8 YGLGSSAAVLVS | سر سر | Db Qy |
| | ILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAK 179 YAKSCDIAMKHFHLTIDSNLDDSNG | 20 LQGLDITILGSNDFY | ь | Db Qy |
| | TLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119 : | 63 PQLSRESMYKLSLNHLTLQSVSASDS :: : : : 48IHSKALHHNPVTFSRDEDS | | Db Db |
| | VLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWIDVKLTS 62 | 3 VVASAPGKVLMTGGYLVLEKP : : : 2 IQVKAPGKLYIAGEYAVTE-P | р ү | Db Qy |
| 23; | | Match Local Similarity Es 103; Conservat | Query Best Lo Matche | |
| | Pmev_kin_Gr_pos; i. 0203 MW; 67EF432FA155FFE5 CRC64; | TIGREAMS; TIGROIZZO; Kinase SEQUENCE 358 AA; 4 | • | w z c |
| | | InterPro; IPR001459; Pfam; PF00288; GHMP PRINTS; PR00959; MEV | | 0000 |
| | ntiality of the mother in gram-position | cation nteny lol. 90087 | 4 PM C4 PM = | מַמִּמִטּט |
| | ed=10894743; R., Bryant A.P., Chalker A.F., Holmes D scu S., So C.Y., Rosenberg M., Gwynn M. | FROM N.A. 20353468; 2.I., Brow K.A., Ior | H≅⊠∽ | מתתקת |
| | Bacillus/Clostridium group; Bacillales; | Staphylococcus aureus Bacteria; Firmicutes; Staphylococcus. NCBI_TaxID=1280; | - z s = s | R 0 0 0 0 0 |
| | 16, Last se 21, Last an | 1-MAR-2001 (TrEMBLrel. 1-JUN-2002 (TrEMBLrel. hosphomevalonate kinas VAK2. | X 7000 | ១១១១១ |
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| | VESLIQAFKTNNIKGVQKMIRINRRIIQSMDNEASVEI 295 | : : 18 GDFLDQSHAC | b 24 | Дb |
| | IIKELLEAREAML | 50 DVYLRVIKSCSVLTSEKWVLHATEPINEA | у 36 | Ωγ |
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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RA Mizutani Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Mizutani Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
Whole genome sequencing of meticillin-resistant Staphylococcus
Wi Taureus ...
EMBL; AP003159; BAB56754.1; -..
BEMBL; AP003111; BAB41781.1; -..
REMBL; AP003131; BAB41781.1; -..
RINTEPPO; IPR001745; GHMPkhose_ATP,
InterPro; IPR001459; Mev_gal_kin.
R Pfam; PP00288; GHMP_kinases; 1.
R PGINTS; PR00959; MEVGALKINASE.
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Kinase; Complete pro
Kinase; 358 AA;
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Cui L., Oguchi A., Aoki K.-I., Nagai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.aureus (strain Mu50), an MEDLINE=21311952; PubMed=11418146;
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Search completed: April 26, 2003, 12:57:02 Job time : 92 secs

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Result

Database

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| conserved nypothet | hypothetical prote | hypothetical prote | malate oxidoreduct | hypothetical prote | outD protein - Erw | l1beta-hydroxyster | mevalonate kinase | CLB1-like protein | two-component hybr | hypothetical prote | hypothetical prote | probable membrane | probable pre-mRNA | NAD+-protein ADP-r | sulfite reductase |

ALIGNMENTS

C;Accession: C86443

C;Accession: C86443

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Cross-references: GB:AE005172; NID:g11136726; PIDN:AAG31307.1; GSPDB:GN00141 C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 unknown protein [imported] - Arabidopsis thaliana Query Match 100.0%; Score 2581; DB 2; Best Local Similarity 100.0%; Pred. No. 3.8e-191; 301 FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWD FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL Conservative 0; Mismatches Length 505; Indels 0: Gaps 360 300 300 240 240 0

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A;Molecule type: DNA
A;Residues: 1-426 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable phosphomevalonate kinase - fission yeast (Schizosaccharomyces
C; Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL;AL109739; PIDN:CAB52264.1; GSPDB:GN00066; A;Experimental source: strain 972h-; cosmid c343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z21804
A;Accession: T38650
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NVIKTWKDDGVVPMDVSPAFDGLAVE 426
                            KLTQAWSSHNVLALLVREDPHGVCLE 486
                                                                              IRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG--T
| : | | | | | | | | : : :
                                                                                                                                                                                                          WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLEL
                                                                                                                                                                                                                                                                                                                   ----QVHKTGLGSSAAMITSLIGSL--FLSLRRLTDDTGDKSLKIDDSTKVIVHNLAQI
                                                                                                                                                                                                                                                                                                                                                                                                                  SLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAP---FASITFNAAESNG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSPQ-LSRESMYKLSLN------HLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYLRVIKSCSVLTSEKWVLHATEPINEAIIĶELLEAREAMLRIRILMRQMGEAASVPIEP
                                                                                                                                                         ETKLNDLSKLAKDHWDVYLRV---IKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLR 402
                                                                                                                                                                                        WSDV-VPFQLPATYCLLMGDV-AGGSSTPGMVKKVQQWQKENPEESK----NCFD----
                                                                                                                                                                                                                                                      AHCSAQGKVGSGFDVGAATWGSCIYRRFDPKLIEQLLVPYDEQIKNINFSTELRKIVSKK
                                                                                                                                                                                                                                                                          SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV----AVTGLPLNEVIGTILKGK
                                                                                                                                                                                                                                                                                                                                      ANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPC--KEGKFGCSDLDVIHMIAQT
                                                                                                                                                                                                                                                                                                                                                                                    --QPLCWQDLQVTLQVDNAYY-HQPQ-----LKPDQ--TSYPKFNFLNCTLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                KSPQFINAEWLYNIDWTVSPIRVHQIYENCELEKNPNPFVQLALFYVI-NYFFSTGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKVTCSAPGKVLIAGGYIVLDPQYSGLVIGLTAKGYASTTTLDD------KCGTVRV
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                                                           ITV-----EAKVDIEPLKQTNILDNIEQLPGVIGVGVPGAGGFDAQFCLAINHTEIIE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 30.;
53; Conservative
                                                                                                                           ------DLYSRVLSIKNCFL-----SSESLDSELQSQFRSIRRILQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 493; DB 2;
; Pred. No. 4.2e-30;
83; Mismatches 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 426;
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| INTOMOTICES PROCESH REAL PROCESS SET IN THE PROCESS OF THE PROCESS | Qy 460 TKLTQ/ : Db 414 LRAQT/ | Qy 400 MLRIR: 1 1 1 1 1 1 1 1 1 1 | Qy 342 LELETI Db 307 SRFMD | Qy 285WDI : Db 248 EEDWN | QY 232 LAQGKY Db 198 QAQGK | Qy 172 NSKPEV : Db 145 HRIEEV | QY 112 KESLHI :: Db 102 KPNMDI | Qy 56 TDVKL: | Qy 6 SAPGKY Db 8 SAPGKY | Query Match Best Local Sir Matches 155; | A; ACCESSION: A39000 A; Molecule type: DN, A; Residues: 1-212, /, A; Cross-references: C; Genetics: C; Gene: SGD:ERG8 A; Cross-references: A; Map position: 13R C; Keywords: phospho | Experi Tsay, 1. Cel Title: Refere | A;Accession: S5758 A;Molecule type: I A;Residues: 1-451 A;Cross-references | C; Species: Saccharom C; C; Date: 19-Oct-1995 C; Accession: S57588; C; Accession. S57588; R; Skelton, J.; Churc submitted to the EMB A; Reference number: | ate |
|--|---|---|---|--|---|--|--|--|--|--|--|---|---|---|--|
| lision 03-Nov-1995 #text_change 21 'ision 03-Nov-1995 #text_change 21 'ision 03-Nov-1995 #text_change 21 'Ision 03-Nov-1995 #text_change 21 'Ision of ERG8, an essential gene of the property of the prope | AWSSHNVLALLVREDE : ANDKRFSKVQWLDVTQAI | ILMRQMGEAASVPIEPES : : : RSFRKITKESGADIEPPY | <pre>\$LSKLDRLHETHDDYSDQ</pre> | NKRTEFSLPPLMNLFLGE : :: : TIKSNHLPSGLTLWMGI | /GSGFDVSCAVYGSQRY\ - | /AKTGLGSSAAMTTAVV/ : : /PKTGLGSSAGLVTVLTT | <pre>(LLLQGLDITILGSNDFY : : :)YCNRNLFVIDIFSDD</pre> | SPQLSRESMYKLSLNHI | /LMTGGYLVLEKPNAGL\ : : \LLAGGYLVLDTKYEAF\ | | A R',214-417 EMBL:M636 SGD:S0004 | binson, G.W. 11, 620-631, 199 and characterize ser: A39606; MUID: | 7588 DNA 51 <ske> Ses: EMBL: Z49939;</ske> | paromyces cerevisi 1995 #sequence_rev 1588; #39606 Churcher, C.M. EMBL Data Librar Der: S57587 | N; Alternate names: protein YM9959.02; |
| #text_change 21 #text_change 21 ### ### #### ###################### | | SQTQLLDSTMSAEGVLL : : VQTSLLDDCQTLKGVLT | RVIKSCSVLTSEKWV :: : : : : DIFESLERNDCTCQKY- | EPGSGGSSTPSMVGAVK ; : DI-KNGSETVKLVQKVK | RESPEVLSFAQVAVTG :: RREPPALISN | AALLHYLGVVDLSDPCK : : : : | YSYRNQIESAGLPLTPE | FIP | /LSTNARFYAIVKPINE : : : : /VGLSARMHAVAHPYGS | Score 453.5; I Pred. No. 5.1e- 2; Mismatches | 22,'D',4; 553127; 1 :YMR220w | of E 7228; | g887599; F | ion 03-Nov- June 1995 | 2; protein |
| | | AGVPGAGGEDAIFAITL | LHATEPINEAIIKELLEAREA : : PEITEVRDA | KWQMSDPEKARĖNWQNL | LPLNEVIGTILKGK ; ; ; LPDIGSATYGSKLAHLVD | EGKFGCSDLDVIHMIAQTSHC : : : KYREVIHNLAQVAHC | SLGTLAPFASITFNAAESNGA | PFVEHAIQYAIAAAHLAT : : PFIEKVIANVFSYF | EVKPESWAWK- :: : LQGSDKFEVRVKSKQFKD | 2; Length 7; 85; Indels | 1596.1; | ial gene | g887601; MIPS | #text_change | W072 |

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D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                        mevalonate kinases homolog lin0012 [imported] - Listeria innocua (strain Cl C;Species: Listeria innocua C:Species: Listeria innocua C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AE1434
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AE1434
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                                                            R;Glaser, P.; Frangeul, L.; Buchrieser, C.;
.; Dominguez-Bernal, G.; Duchaud, E.; Durand
D.; Jones, L.M.; Karst, U.
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A; Residues: 1-323 <KUR>
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A; Accession: F90479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision
C;Accession: F90479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE006641;
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                                                                                                                                                                                                                                                                                                                                                                                                                         --MNLFLGEPGSGGSSTPSMVGAVKKW-QMSDPEKARENWQNLSDANLELETKLNDLSKL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSPQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVASAPGKVLMTGGYLVLEKPNAGL--VLSTNARFYAIVKPINEEVKPESWAWKWTDVKL
                                                                                                                                                                                                                             IIDVKED-EGLRLES
                                                                                                                                                                                                                                                          ALLVREDPHGVCLES
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                                                                                                                                                                                                                                                                                                                                                                                                        GNYDMMLGFTGKSSET----VGLVRKFVEKSNLDDFKEIMRLIDEENY-MAIKLIKLNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFDIASAVFGSIVYKRFT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGLGSSSAATVSLTACLYYAI - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKVSAPGKILWIGSYSVV----FGGISHVIAVNKRVSCSLREIKE-
                                                                                                                                                                                                                                                                                                                 AASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFLAIFAITLGDSGTKLTQAWSSHNVL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110;
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Pred. No. 5.3e
72; Mismatches
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                                                                          Durand,
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species.
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                                                                         A.; Baquero,
Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DLDKMDFYFEKLNL
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                                                                         , F.; Bercl
.; Entian,
               ΙΟ, Ε.;

J.A.;
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                                                                                                                                                  (strain Clip11262)
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                                                                         Berche, P.;
Lian, K.D.;
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                             Maitournam,
               Voss,
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H.P.; Redd
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Fsihi, H.
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Wehland,
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A;Cross-references: GB:NC_003210;
A;Experimental source: strain EGD
C;Genetics:
A;Gene: lmo0012
                                                                                                                                              A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-FA;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AB1806
                                                                                                                                                                                                                                                                                                                                      mevalonate kinases homolog lmo0012 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-C;Accession: AE1806
                                                                                                       A; Molecule type:
                                                                                                                                                                                                                                                       Science 294, 849-852,
                                                                                                                                                                                                                                                                                               R;Glaser, P.; Frangeul, L.; Buchrieser, C.; A.; Dominguez-Bernal, G.; Duchaud, E.; Durand,
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A;Experimental source: strain Clipl1262
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A; Residues: 1-360 <GLA>
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A;Accession: AE1434
A;Status: preliminary
                                                                                   A; Residues: 1-359
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                                                               PIDN: CAC98227.1;
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d, L.; Dussurget, O.;
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| | QY 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62 | Query Match 5.2%; Score 134.5; DB 2; Length 358; Best Local Similarity 21.8%; Pred. No. 0.015; Matches 104; Conservative 59; Mismatches 181; Indels 133; Gaps 23; | strain N315 | liminary pe: DNA -358 <kur> ences: GB:</kur> | A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: B89828 | R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. | B89828 phosphomevalonate kinase [imported] - Staphylococcus aureus (strain N315) c;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Cares:ion. R89828 | 7 | Qy 465 AW 466 Dh 339 FW 340 | QY 407 MRQMGEAASVPIEPESQTOLLDSTMSAEGYLLAG-VPGAGGEDAIFAIT-LGDSGTKLTQ 464 Db 286GTKAGVNIETSLLKELADSAENMGGAGKSSGSGGDDCGTAFSKTKELAEKLVN 338 | 251 RNNEIMKQIIQAFHTKDEELLYSAIKENRRILQEL | Db 203 MLQIETLEEPVPTFSVGWTGT-PVSTGKLVSQIHAFKQEDSKNYQHFLT 250 OV 347 KLNDLSKLAKDHWDVYLRVTKSCSVLTSEKWVLHATEPTNEATTKELLEAREAMT.BTRTL 406 | QY 287 NKRTEFSLPPLMNLFLGEBGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELET 346 | 227 QTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWD | QY 169 NGANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIA 226 : | 88IIETELIDQ | 72 DGEHWTETAEAINIAT | 8 PGKVLMTGGYLVLEKPNAGLVKSTNARRYAIVK | Query Match 5.8%; Score 149.5; DB 2; Length 359; Best Local Similarity 20.5%; Pred. No. 0.001; Matches 99; Conservative 60; Mismatches 146; Indels 177; Ga | |
|--|--|---|--|--|--|--|--|---------|---|--|--|---|---|--|---|---|---|---|--|---|
| Qy 293 SLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSD 339 | 253 YVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEF | | 169 NGANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKE | | Qy 68 ESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKL-LL 120 : : | Query Match 5.0%; Score 130; DB 2; Length 816; Best Local Similarity 19.0%; Pred. No. 0.13; Matches 106; Conservative 76; Mismatches 203; Indels 174; Gaps 21; | A; dene: CESP:F33H2.2 A; Map position: 1 A; Map position: 1 A; Introns: 51/1; 101/3; 186/1; 270/3; 328/2; 380/3; 509/2; 751/2 C; Superfamily: Caenorhabditis elegans hypothetical protein F33H2.2 | . 5 fi. | A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A.Besidines: 1-816 (MIT) | R:Cottage, A. submitted to the EMBL Data Library, November 1996 A;Reference number: Z19463 A;Accession: T21713 | Caenorhabditis elegans -Oct-1999 #sequence_revision 15-Oct-1999 #text_change n: T21713 | RESULT 8 T21713 To the first brotein F33H2.2 - Caenorhabditis elegans | Db 296 ETEKLKYLCDIAEKYHGASKTSGAGGGDCGITIINKDVDKEKIYDEWTKHGIKPL 350 | KLTQAWSSHNVLAL 474 | 359 WDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAML | QY 299 NLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDH 358 : | Qy 241 FDVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLM 298 | QY 181 GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240 | 123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKT | Db 36 ATIEEADQYKGTIHSKALHHNPVTFSRDEDSIVISDPHAAKQ 77 |

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RESULT 9
F70185
phosphomevalonate kinase homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change
C:Accession: F70185
C:Accession: F70185
C:Accession: S,; Huang, W.M.; Sutton, G.G.; Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat Nature 390, 580-586, 1997
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A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID:98065943; PMID:9403685
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A; Residues: 1-317 <K
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Best Local :
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                                                                                                                                                                                                                                                                                              126 TILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGLGSS
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                                                                                                                                                                                                                                      AAMTTAVVAALL----HYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCL-----AQGKV
                                                                                                                                                                                                                                                                    --LSQNCFFNLEN----
                                                                                                                                                                                                                                                                                                                                                         SRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQGLDI
                                                                                                                                                                                                                                                                                                                                                                                      SVPGNLLLMGEYTILEEKGLGLAIAINKRAFFSFK-
                                                                                                                                                                                                                                                                                                                                                                                                              SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTSPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOSFQHHRFLVSSTKHEPH
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IEPE----SQTQLLDSTMSAEGVLLAGVPGAGGFD--AIFAITLGDSGTK 461
                           HRNSILDFILKCN-LEMKKLVLNASNS-KSALISSLRRAKELGLAIG---EAIGVSAALP
                                                       HWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVP
                                                                                                                 MNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKD
                                                                                                                                                 GSGYDIATSIFGG----
                                                                                                                                                                           GSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QSVPLIGPPNAETCSPWFRLSIYSACSSGPPSVFLPHGTRLTTLPRV
                                                                                                                                                                                                                                                                                                                             ----KIDDFSLIENRSDFVFKMFAY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.8%;
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                                                                                                                                                 ---VIEF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 124.5; DB 2;
Pred. No. 0.072;
""" ematches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g2688611;
                                                                                     MQGLQ -- AIKTTTSICEYNK ----
                                                                                                                                                                                                                                                                                                                                                                                      -KSDSWRF
                                                                                                                                              -EGGFNPKCRQLGAVEF
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Vugt,
B.
          A; Note: Nostoc sp. strain PCC 7120 is a synonym of C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 C; Accession: AIZ447 C; Kraneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
                                                                                                   RESULT
AI2447
                                                                 hypothetical protein C; Species: Nostoc sp.
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 (;Accession: S42088 R;Riou, C.; Tourte, Y.; Lacroute, F.; Karst, F. submitted to the EMBL Data Library, February 1994 A;Description: Isolation and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: \tilde{A}TP; isoprenoid biosynthesis; phosphotransferase F;330-339/Region: ATP binding #status predicted F;352/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mevalonate kinase (EC 2.7.1.36)
C; Species: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Pathway: isoprenoid biosynthesis A; Note: this enzyme can also utilize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-378 <RIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: catalyzes the reversible phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X77793; NID: g456613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: $42088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Superfamily: mevalonate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                IHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSPQLSRESMYKLSLNHLTLQSVSASDSRN-PFVEHAIQYAIAAAHLATEK--DKESLHK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEVKARAPGKIILAGEHAVVHG-----ST----AVAAAID-----
                                          RIRILMROMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITIGDSGT
                                                                                                                                        LELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAML
                                                                                                                                                                                                                                                                                      LNKWAFEGEKIIHGK-PSGIDNTVSAYGN------MIKFCSGEITRLQSNMPLRMLI
                                                                                                                                                                                                                                                                                                                                                                                                                               AAESNGANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSD - - - LDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGT-LAPF--
                                                                                                                                                                                                                                       KGKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDAN
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LSMGVSHSSIEAVILTTVKHK--LVSKLTGAGGGGCV--LTLLPTGT
                                                                                                                                                                                                                                                                                                                                                                               SGLGSSAALCVALTAALL----ASSISEKTRGNGWESLDETNLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VEEQNLPKEKMWLSSGISTFLWLYTRIIGFNPATVVIN
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Pred. No. 0.13;
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                                                                                                                                                                                       GRNTKALVSGVSQRAVRHPDAMKSVFNAVDSIS
                                                                                           ---TEK--
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protein all5137 [imported] -

Nostoc

sp. (strain

PCC

Anabaena sp. #text_change

strain PCC 30-Jun-2002

Sasamoto,

Yamada,

S.; Watanabe, , M.; Yasuda,

; Irigu Tabata

Shimpo, S.;

Y.; Wolk, C.P.; Kuritz, T.; Sa: S.; Sugimoto, M.; Takazawa, M.;

ATP

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R;Schafer, B.L.; Bishop, R.W.; Kratunis, V.J.; Kalinowski, J. Biol. Chem. 267, 13229-13238, 1992
A;Title: Molecular cloning of human mevalonate kinase and A;Reference number: A42919; MUID:92317034; PMID:1377680
A;Accession: A42919
                                                                                                                A; Molecule type: mRNA
A; Residues: 1-396 <SCH
A; Residues: 1-396 <SCH
A; Rosidues: GB: M88468; NID: 9307197; PIDN: AAB59362.1;
A; Note: sequence extracted from NCBI backbone (NCBIN:107743,
R; Graef, E.; Caselmann, W.H.; Wells, J.; Koshy, R.
                                                                                                                                                                                                                                                                                         mevalonate kinase (EC 2.7.1.36) - human

%;Alternate names: MK

G;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence_revision 18-Mar-1997 #text_change 11-Jun-1999

C;Accession: A42919; A58527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
A;Reference number: AB1807
A;Accession: AI2447
                                                                                                 R;Graef, E.; Caselmann,
Oncogene 9, 81-87, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-721 < KUR>
                                                       A; Accession:
                                                                     A; Reference number: S42226;
                                                                                                                                                                                                                                                                                                                                                                                 A42919
                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                     :Residues: 1-396
   Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
                                                     A58527
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                                     mRNA
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                   <GRA>
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   EMBL: x75311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GAEGAILAIEEDGKTAQVWLDGLP----AQVLENYGTNSR-+FTLAT
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22.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSRTGLIAKAQFSKVTETIPLQVGQLIQENVRVLSRNINLILAL
                                                                     MUID:94134441;
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NID:g450345;
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                                                                     mevalonate kinase by
4134441; PMID:8302606
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 PIDN:CAA53060.1;
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                                                                                                                                                                                                                                                                            Kalinowski,
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                                                                                   hepatitis
                                                                                                                                                                                                                                          identification of a
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                                                                                                                                     PID: g187561
NCBIP: 107744)
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PID: 9450347
                                                                                                                                                                                                                                                                         Mosley,
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                                                                                     B virus
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C;Genetics:
A;Gene: GDB:MVK
A;Cross-references: GDB:134189; OMIM:251170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: this enzyme can also utilize GTP, C; Superfamily: mevalonate kinase
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A; Note: defects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Pathway: isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: catalyzes the reversible phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function
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357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defects in this gene can cause mevalonic aciduria
KQALTSCGFD-----CLE----TSIGAPGVSIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLYSAPGKVILHGEHAVVH-GKVALAVSLNLRTFLRLQPHSN------GKVDLSL 53
                                HNVLALLVREDPHGVCLESGDPRTTCITSGVSSIH
                                                                                                   {\tt QMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSS}
                                                                                                                                       GEMGE-
                                                                                                                                                                         NDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR
                                                                                                                                                                                                                                        RTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKL
                                                                                                                                                                                                                                                                            GERMIHGN-PSGVDNAVSTWGG---
                                                                                                                                                                                                                                                                                                             SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNK 288
                                                                                                                                                                                                                                                                                                                                             WSELPPGAGLGSSAAYSVCLAAALLTV--CEEIPNPLKDGDCVNRWTKEDLELINKWAFQ
                                                                                                                                                                                                                                                                                                                                                                              -----KTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEG----KFGCSDLDVIHMIAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                               LDITILGSNDFYSYRNQIESAGLP---LTPESLGTLAPFASITFNAAESNGANSKPEVA- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNIGIKRAWDVA----RLQSLDTS-----FLEQGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
                                                                  ----ALGVGHASLDQLCQVT-RARG-LHSKLTGAGGGGC--GITLLKPGLEQPEVEAT
                                                                                                                                                                                                           -TNTKVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5%;
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                                                                                                                                                                                                          --RNTRALVAGVRNRLLKFPEIVAPLLTSIDAISLECERVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 117;
Pred. No. 0.
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                                                                                                                                                                                                                                                                            ---ALRYHQGKISSLKRSPALQILL-----
                                                                                                                                       APAPEQYLVLEELIDMNQHHLN-----
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RESULT 13

C; Keywords: phosphotransferase F; 1-157/Region: hepatitis B vii F; 162-557/Region: human mevalor A; Molecule type: mRNA A; Residues: 1.557 <GRA> A; Title: Insertional activation of mevalonate kinase by A; Reference number: S42226; MUID:94134441; PMID:8302606 A; Accession: S42226 R;Graef, E.; Caselmann, Oncogene 9, 81-87, 1994 C;Date: 13-Jan-1995 #sequence_revision 17-Mar-1997 C;Accession: S42226 A; Cross-references: EMBL: X75311; NID: g450345; PIDN: CAA53059.1; hypothetical large surface antigen/mevalonate kinase Species: hepatitis B virus, W.H.; Wells, mevalonate virus large J.; Koshy, surface antigen (fragment) #text_change OEC hepatitis 2.7.1.36) mutant fusion PID:9450346 20-Oct-2000 B virus DNA ä prot

| Qy 3 VVASAPGKVLMTGGY-LVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTD 57 | Query Match 4.5%; Score 116; DB 2; Length 335; Best Local Similarity 21.9%; Pred. No. 0.36; Matches 102; Conservative 60; Mismatches 124; Indels 180; Gaps 25; | A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A; Reference number: A71000; MUID:98344137; PMID:9679194 A; Accession: A71042 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-335 KAN> A; Cross-references: GB: AP000006; NID:g3236133; PIDN:BAA30737.1; PID:g3258054 A; Experimental source: strain OT3 A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics: A; Gene: PH1625 C; Superfamily: galactokinase | A71042 probable mevalonate kinase - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000 C;Accession: A71042 R;Kawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S; Sekin M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi DNA Res, 5, 5,76, 1998 | QY 469 HNVLALLVREDPHGVCLESGDPRTTCITSGVSSIH 503 Db 518 KQALTSCGFDCLETSIGAPGVSIH 541 RESULT 14 | Qy 349 NDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR 408 :: : | Qy 229 SHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNK 288 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : | Qy 123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVA- 178 | Query Match 4.5%; Score 117; DB 4; Length 557; Best Local Similarity 20.2%; Pred. No. 0.68; Matches 104; Conservative 74; Mismatches 183; Indels 154; Gaps 22; Qy 3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62 : |
|--|--|--|---|--|--|--|--|---|
| Qy 305 -PGSGGSSTPSMVGAVKKWOMSDPEKARENWQNL 337 | QY 252 RYVRESPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEPSLPPLMNLFLGE 304 | FVEHAIQYAIAAAHLATEKDKESLHKLLLQGLDITILGSNDFYSYRNQIE 141 | | A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: B86705 A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-816 <sto> A:Cross-references: GB-AFR05176: PID:d12723546: PID:AAK04740 1: GSPDB-GN00146</sto> | — | Db 232 ÅK | Db 156 G-ASSGIDPTVSAVGGFLYXKQKREEP | Db 62 VSFSEDKIYFETDYGKAAEVLSYVRYAIELALEESDKR 99 Qy 118 LLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITENAAESNGANSKPEV 177 |

| Вþ | 357 | 357 SPDEAIAILQGLREKFEDYHQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAV 416 | • |
|----------------|-------------|--|---|
| Qy | 389 | SV | |
| Ф | 417 | 417 KISVKNQQTKRLDLEKELTEAQEELSEAVIKLDIKASRTKEKAVEKIADKIYKFSVKEDK 476 | |
| Qy | 423 | 423 QTQLLDSTMSAEGVLLAGVP 442 | |
| Вb | 477 | 477 ROEVTDOAVVAVASTLIGVP 496 | |
| Searc Job t | h co ime | Search completed: April 26, 2003, 12:57:30 Job time : 26 secs | |
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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1496.110 Million cell updates/sec
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                                                               SwissProt_40:*
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   DHILMOUSE
FTSH_CAPAN
NXIA_MOUSE
YJSP_YEAST
ALT_BPT6
KIME_ARCFU
LDHA_BRARE
GALL_CANPA
GSOD_ERWCH
PPB_SERWA
DHILHUMAN
ALT_BPT2
KIME_UCOLI
FIAL_USTMA
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FIXL_BRAJA
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KIME_ARATH
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Q9nri5 homo sapien
Q9nrk1 clostridium
Q9be24 macaca fasc
Q92974 homo sapien
P27395 j genome po
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Q03426
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P51975 ovis aries
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Q9v187 pyrococcus
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ERG8_YEAST
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| 4.5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | <u>ა</u> | 34 | |
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| 92.5 | 93 | 93 | 93 | 93.5 | 93.5 | 94 | 94 | 94 | 94.5 | 94.5 | 94.5 | |
| 3.6 | 3.6 | 3.6 | 3.6 | 3.6 | 3.6 | 3.6 | 3.6 | 3.6 | 3.7 | 3.7 | 3.7 | |
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| DPO1_RICFE | ECHA_PIG | EF2_METTH | GSPD_ERWCH | XYNA_THESA | GAL1_CANAL | POLG_JAEV5 | DNBI_HSVEB | MBHL_RHOGE | NF1_MOUSE | IF2C_GUITH | YYXA_BACSU | |
| Q9raa9 rickettsia | | 027131 methanobact | | P36917 thermoanaer | P56091 candida alb | P19110 j genome po | .P28932 equine herp | P17632 rhodocyclus | Q04690 mus musculu | | | • |

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Matches
                                                                      MEDLINE-20252529; PubMed-10794536; Lluch M.A., Masferrer A., Arro M., Boronat "Molecular cloning and expression analysis gene from Arabidopsis thaliana."; Plant Mol. Biol. 42:365-376(2000).
                                                                                                                                                            "Isolation and characterization of a cDNA encoding Arabidopsis thaliana mevalonate kinase by genetic complementation in yeast Gene 148:293-297(1994).
                                                                                                                                                                                                           STRAIN-cv. Landsberg erecta; TISSUE-Leaf; MEDLINE-95047438; PubMed-7958957; Riou C., Tourte Y., Lacroute F., Karst F.
                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mevalonate kinase (EC 2.7.1.36) (MK)
                                                                                                                                                                                                                                                                                                                                                                                                         KIME_ARATH P46086;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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               phosphomevalonate.
ENZYME REGULATION:
PYROPHOSPHATE (GPP)
                                                         CATALYTIC ACTIVITY: ATP + (R)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRIEEVPKTGLGSSAGLVTVLTTALASFF-VSDLENNVDKYR-----EVIHNLAQVAHC
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Pred. No. 1.8e-26;
'2; Mismatches 185;
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                 IS INHIBITED IN
L PYROPHOSPHATE
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                                                                                                                                                                                                                                                                                                          eudicots;
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                              VITRO
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udicots; Rosidae;
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KIME_HUMAN
ID KIME_H
AC Q03426
DT 01-OCT
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DT 15-JUN
DE Mevvalo
GN MVK.
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Best Local :
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01-OCT-1993
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or send a
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NP_BIND 141 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGR00549; mevalon_kin; 1. PROSITE; PS00627; GHMP_KINASES_ATP;
                               Mevalonate kinase
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PRINTS; PR00959; MEVGALKINASE.
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InterPro; IPR001459; Mev_gal_kin.
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 iomo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (S send an email to license@isb-sib.ch).
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PATHWAY: CHOLESTEROL BIOSYNTHESIS, MEVALONATE CATABOLISM.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY
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                                                                                                                                                                                                    RIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGT
                                                                                                                                                                                                                                                                                                                                         LNKWAFEGEKIIHGK-PSGIDNTVSAYGN-----MIKFCSGEITRLQSNMPLRMLI
                                                                                                                                                                                                                                                          LELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAML
                                                                                                                                                                                                                                                                                                                    KGKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDAN
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(Rel.
(Rel.
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  (Human).
                                                                                                     STANDARD;
                          27, Created)
27, Last sequence 41, Last annotations (EC 2.7.1.36)
                                                                                                                                                                          LSMGVSHSSIEAVILTTVKHK--LVSKLTGAGGGGCV--LTLLPTGT
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151 ATP (POTENTIAL)
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                             Last sequence up Last annotation 2.7.1.36) (MK).
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B; Mismatches
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Pred. No. 0
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                                                           update)
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                                           update)
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Gibson K.M., Wanders R.J.A., Waterham H.R.;
"Organization of the mevalonate kinase (MYK) gene and identification of novel mutations causing mevalonic aciduria and hyperimmunoglobulinaemia D and periodic fever syndrome.";
Eur. J. Hum. Genet. 9:253-259(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mosley S.T., Gibson K.M., Tanaka R.D.;
"Molecular cloning of human mevalonate kinase and identification missense mutation in the genetic disease mevalonic aciduria.";
J. Biol. Chem. 267:13229-13238(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinson D.D., Ross R.M., Krisans S., Shaw J.L., Kozich V., Rolland M.-O., Divry P., Mancini J., Hoffmann G.F., Gibson K.M.; "Identification of a mutation cluster in mevalonate kinase deficiency, including a new mutation in a pattent of Mennonite ancestry.", am. J. Hum. Genet. 65:327-335(1999).
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MEDLINE=94134441; PubMed=8302606;
                                        VARIANTS HIDS
S-309; R-326 P
                                                                                                                                                                                                Drenth J.P.H., Cuisset L., Grateau G., Vas. van der Velde-Visser S.D., de Jong J.G.N.,
                                                                                                                                                                                                                                               VARIANTS HIDS LEU-167; THR-268 AND ILE-377. MEDLINE-99295936; PubMed-10369262;
                                                                                                                                                                                                                                                                                                                  "Mutations in MVK, encoding mevalonate kinase, hyperimmunoglobulinaemia D and periodic fever: Nat. Genet. 22:175-177(1999).
                                                                                                                                                                                                                                                                                                                                                               Poll-The B.T.; "Mutations in MVK,
                                                                                                                                                                                                                                                                                                                                                                                                                               VARTANTS HIDS PRO-20: THR-268 AND ILE-377.

MEDLINE-99295935; PubMed-10369261;

Houten S.M., Kuis W., Duran M., de Koning T.J., van Royen-Kerkhof

Romeijn G.J., Frenkel J., Dorland L., de Barse M.M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99330561; PubMed=10401001;
Houten S.M., Romeijn G.J., Koster J., G.
Smit G.P.A., de Klerk J.B.C., Duran R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS MEVALONICACIDURIA ILE-243; PHE-264; PRO-265
MEDLINE-99347937; PubMed-10417275;
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Caruso U., Landrieu P., Kelley R.I., Kuis W., Poll-The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                       Huijbers W.A.R., Rijkers G.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and characterization of three novel missense mutations in mevalonate kinase cDNA causing mevalonic aciduria, a disorder of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS MEVALONICACIDURIA MET-310 AND THR-334
MEDLINE-21214738;
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9:81-87(1994).
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                                                                                                          in the gene encoding ever syndrome."; 22:178-181(1999).
                                        N-20; P-20; P-39;
AND I-377, VARIANT
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Gibson K.M., Tanaka R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8:1523-1528(1999).
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MEVALONICACIDURIA
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                                                                                                                                                                                                                                                                                                                                                                                                            Waterham
                                        L-150; L-167; R-202; Q-215; T-268; MEVALONICACIDURIA T-334, AND VARIA
                                                                                                                                                       mevalonate kinase cause hyper-IgD
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URIA P-
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-20; F-264; T-268;
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e B.T.,
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Cuisset L., Drenth J.P.H., van der Velde-Visser S.D., Delpech M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.com/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/li
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Eur. J. Hum. Genet. 9:260-266(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal.
DISEASE: DEFECTS IN MYK ARE THE CAUSE OF MEVALONICACIDURIA.
AN ACCUMULATION OF MEVALONIC ACID WHICH CAUSE A VARIETY OF
SYMPTOMS SUCH AS PSYCHOMOTOR RETARDATION, DYSMORPHIC FEATURE
CATARACTS, HEPATOSPLENOMEGALY, LYMPHADENOPATHY, ANEMIA, HYPO
MYOPATHY, AND ATAXIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: DEFECTS IN MVK ARE THE CAUSE OF HYPERIMMUNOGLOBULINEMIA AND PERIODIC FEVER SYNDROME (HIDS); AN AUTOSOMAL RECESSIVE DISEAS CHARACTERIZED BY RECURRENT EPIDOSES OF UNEXPLAINED HIGH FEVER ASSOCIATED MITH SKIN RASH, DIARRHEA, ADENOPATHY (SWOLLEN, TENDER LYMPH NODES), AND ATHRALGIAS AND/OR ARTHRITIS. CONCENTRATION OF IGD, AND OFTEN IGA, ARE ABOVE NORMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphomevalonate.
ENZYME REGULATION: FAR
COMPETITIVE INHIBITORS
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InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1. MIM; Genew; PIR; A42919; A42919 EMBL; EMBL; EMBL; EMBL; EMBL; VARIAN VARIANT VARIANT Peroxisome; Transferase; PRINTS; PR00959; MEVGALKINASE EMBL; AF217535; AAF82407.1; AF217528; AAF82407.1; AF217529; AAF82407.1; AF217530; AAF82407.1; AF217531; AAF82407.1; AF217532; AAF82407.1; AF217533; AAF82407.1; AF217533; AAF82407.1; 260920; AF217534; HGNC: 7530; TIGR00549; Disease 138 148 135 ; AAB59362.1; ; CAA53060.1; ; CAA53059.1; 52 39 Kinase; Cholesterol biosynthesis; ATP-binding; 20 20 AAF82407 148 20 52 39 mutation; 20 mevalon_kin; _KINASES_ATP; ALT_INIT JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphomevalonate.
-:- COFACTOR: MAGNESIUM (BY SIMILARITY).
-:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-:- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
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DNA Res. 5:55-76(1998).
-!- CATALYTIC ACTIVITY: ATP + (R)-mevalonate =
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InterPro; IPR001459; Mev_gal_Kin.
Pfan; PF00288; GHMP_kinases; 1.
PRINTS; PR00959; MEVGALKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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Smit G.P.A.,
Waterham H.R.
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                                                                                                                                                                 InterPro; IPR001745; GHMPknse_ATP
InterPro; IPR001174; Galkinase.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99330561; PubMed=10401001;
                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        modified
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Mammalia; Eutheria;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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TIGREAMS; TIGR00549; mevalon_kin; 1.
PROSITE; PS00627; GHMP_KINASES_ATP;
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Hum. Mol. Genet. 8:152
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                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exeropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal.

SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPETITIVE INHIBITORS (BY SIMILARITY).
PATHWAY: CHOLESTEROL BIOSYNTHESIS, MEVALONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphomevalonate.
ENZYME REGULATION: FARNESYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP +
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2.7.1.36) (MK).
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.B.C., Duran R.,
    MW;
ATP (POTENTIAL).
953DB1C89403A3F8 CRC64;
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Sciurognathi; Muridae;
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SEQUENCE OF 1-40.
MEDLINE=86278718; Pul
Monder C., Shackletor
Iohan F., Lakshmi V.;
"The syndrome of appa"
                                                                                                                         "Differential promoter usage by t
dehydrogenase gene.";
Mol. Endocrinol. 6:1082-1087(1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Corticosteroid 11-beta-dehydrogenase, isozy
(11-beta-hydroxysteroid dehydrogenase 1) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHI1_RAT P16232;
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                                                                                                                                                                                                    MEDLINE=92375101; PubMed=1508221; Moisan M.P., Edwards C.R., Seckl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                SEQUENCE OF 1-69 I
MEDLINE=92375101;
                                                                                                                                                                                                                                                                                                                      dehydrogenase
                                                                                                                                                                                                                                                                                                                                            Agarwal A.K., Monder C., Eckstein B. "Cloning and expression of rat cDNA
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90037015; PubMed=2808402;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                         "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                 264:18939-18943(1989).
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                                                                                                                                                                                                                                                     FROM N.A
    apparent mineralocorticoid
                                                                                                                                       6:1082-1087(1992).
                                                                      PubMed=3460996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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                                                 C.H.L.,
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Pred. No. 0.43;
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                                                 Bradlow
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                                                                                                                                                                                                           J.R.;
                                                                                                                                                                                                                                                                                                                                                              В.,
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1) (11-beta-HSD1).
                                                 H.L.,
                                                                                                                                                                                                                                                                                                                                                                 White P.C.;
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Best Local S
Matches 52
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ACT_SITE
MUTAGEN
MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                   KIME_PYRAB Q9V187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta ...
"Tyr-179 and Lys-183 are ...;
hydroxysteroid dehydrogenase.";
hydroxysteroid dehydrogenase.";
hydroxysteroid dehydrogenase.";
hydroxysteroid dehydrogenase.";
hydroxysteroid dehydrogenase.";
Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J05107; AAA40886.1; -. EMBL; S43333; AAB22993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The property of the state of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with 11 beta-dehydrogenase and 5 beta-reductase consequences for corticosteroid metabolism.";
J. Clin. Endocrinol. Metab. 63:550-557(1986).
                         MVK OR
                                             Mevalonate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obeid J., White P.C.; "Tyr-179 and Lys-183 are essential for enzymatic activity of 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93038663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGENESIS OF TYR-179 AND LYS-183.
                                                                    L6-OCT-2001
                                                                                      6-OCT-2001
                                                                                                               6-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: LIVER, PTM: GLYCOSYLATED.
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een the Swiss Institute of Bioinformatics and the E
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
-i- CATALYTIC ACTIVITY: ATP + (R)-mevalonate.
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InterPro; IPR001174; Galkinase.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Kinase; ATP-binding; Magnesium; Complete NP_BIND 111 121 ATP (POTENTIAL).
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PRINTS; PR00959; MEVGALKINASE.
TIGRFAMs; TIGR00549; mevalon_kin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR00549; mevalon_kin; lprosite; ps00627; GHMP_KINASES_ATP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a
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SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE
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SUBUNIT: HOMODIMER (BY SIMILARITY).
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GEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHN
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                                                                                                        SKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMR-QM
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                                                                    Query Match
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O1-AUG-1990 (Rel. 15, C
O1-AUG-1990 (Rel. 15, L
16-OCT-2001 (Rel. 40, L
Meyalonate kinase (EC 2
                                                                                                 NP_BIND
                                                                                                                                                                 InterPro; IPR001745; GHMPknse_ATP
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
                                                                                                                    Peroxisome.
                                                                                                                              Transferase;
                                                                                                                                        PROSITE; PS00627;
                                                                                                                                                                                               EMBL; M29472; AAA41588.1; -. PIR; A35629; A35629.
                                                                                                                                                                                                                           entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                'Molecular care,';
levels in rat liver.";
levels in Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinson G.W., Mosley S.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90222132; PubMed=2158094;
Tanaka R.D., Lee L.Y., Schafer B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                                                                                                                                               FIGREAMS;
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   63
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                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. MEVALONATE KINASE
                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic and peroxisomatic DISEASE: MUTATION IN THE MEVALONATE KINASE GENE
                                                                                                                                                                                                                                                                                                                                                          SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                PATHWAY: CHOLESTEROL BIOSYNTHESIS, MEVALONATE CATABOLISM
                                                                                                                                                                                                                                                                                                                                                                            COMPETITIVE INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                     phosphomevalonate.
ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: MAY BE A REGULATORY SITE
                                                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY
                    LLVSAPGKVILHGEHAVVH-GKVALAVALNLRTFLVLRPQSN--
                                      VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
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PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
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                                                                                                                          PR00959; MEVGALKINASE.
is; TIGR00549; mevalon_kin; 1.
;; PS00627; GHMP_KINASES_ATP; 1.
rase; Kinase; Cholesterol biosynthesis;
                                                                  Similarity
                                                                                                 138
395 AA;
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                                                           Conservative
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41987 MW;
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                                                           67;
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                                                                                                ATP (POTENTIAL).
803D1F44E3C525FC
                                                        Pred. No. 0.61
; Mismatches
                                                                             Score 111.5;
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Sciurognathi; Muridae
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                                                                                                 Voice M.W.
                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                           Mus musculus
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            FAMILY
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MEDLINE=95154291; PubMed=/83150.,
MEDLINE=95154291; PubMed=/83150.,
Oppermann U.C.T., Netter K.J., Maser E.;
Cloning and primary structure of murine 11
dehydrogenase/microsomal carbonyl reductase.
T. Blochem. 227:202-208(1995).
                                                               Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: CATALYZES REVERSIBLY THE CONVERSION OF CO
INACTIVE METABOLITE CORTISONE
-i- CATALYTIC ACTIVITY: An 11-beta-hydroxysteroid + NAD
oxosteroid + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95178382; PubMed=7873449;
Rajan V.; Chapman K.E., Lyons V., Jamieson P., Edwards C.R., Seckl J.R.;
"Cloning, segmenting."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P50172;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
corticosteroid 11-beta-dehydrogenase, isozyme 1 (EC 1.1.1.146) (11-DH)
                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, sequencing and tissue-distribution of hydroxysteroid dehydrogenase-1 cDNA.";
J. Steroid Biochem. Mol. Biol. 52:141-147(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
TISSUE SPECIFICITY: SIMILARITY: BELONGS
                                            SUBCELLULAR LOCATION: Microsomal
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                                                                                                                                                                                                        OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
91; PubMed=7851387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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  To
                       WIDELY
  THE
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52:141-147(1995).
  SHORT-CHAIN
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                          EXPRESSED,
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                       HIGHEST EXPRESSION IN LIVER
  DEHYDROGENASES/REDUCTASES
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                                                                                         NADP(+)
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                                                                                                                                                                                                                                                                                                   Q39444;
01-NOV-1997
01-NOV-1997
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        Submitted (AU - ! - FUNCTION:
                                                                                                                        Capsicum annuum (Bell pepper),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; euasterids I; Solanales; Solanaceae; Capsi
                                                                                                                                                                                                                                                                                                                                                                                     CAPAN
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PF00106; adh_short; 1.
TE; PS00061; ADH_SHORT; 1.
reductase; NADP; Microsome
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  , Schantz M.L., Schantz R.;
(AUG-1995) to the EMBL/GenBank/DDBJ
ION: SEEMS TO ACT AS AN ATP-DEPENDENT
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annotation update)
homolog, chloroplast precursor
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Pfam; PF01434; Peptidase_M41;
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X90472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell division; ATP-binding; Transmembrane; Hydrolase;
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COFACTOR: BINDS 1 ZIN
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                        SGNSGVIVLAATNRPDVLDSALLRPGKFDRQVTVDRPDVAGRVRILQVHSRGKALAKDVD
                                            WDNK----RTEFSLPPLMNLFLGEPGSGGSST----PSMVGAVKKWQMSDPEKA-----
                                                                    GVGASRVRHLFENAKSKAPCIVFIDEIDAVGRQRGAGLGGGNDEREQTINQLL-TEMDGF
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                                                                                                                                        KEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDV----
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Bioinformatics Institute. There
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CHLOROPLAST; INTEGRAL MEMBRANE
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Radota K., Matsuda H.A., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schari K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Wombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suruki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Hayashigaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_MOUSE
                                                                                                                                                                                        Submitted (JUN-1998) to the EMPLESSAUL. (1998) to the EMPLESSAULTION: NEURONAL CELL SUCELL RECOGNITION AND CELL
                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                           Gorecki D.C., Szklarczyk A., I
"Differential seizure-induced
                    <del>+</del> <del>+</del>
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                                                                                                                                                                                                                                                         expression."
                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/10;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CD-1; TISSUE-Brain;
Graveley B.R., Philipps D.L.;
"Sequencing of the neurexin g.
Submitted (MAY-2001) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-140 FROM
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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               SUBCELLULAR LOCATION: Type I membrane protein (
ALTERNATIVE PRODUCTS: MULTIPLE ISOFORMS ARE PRO
ALTERNATIVE SPLICING (BY SIMILARITY).
SIMILARITY: CONTAINS AT LEAST 2 LAMININ G-LIKE
SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
                                                                                                                              SUBUNIT: THE SIMILARITY).
                                                                                                                                                                        SIGNALING
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                                                                                                                                                THE CYTOPLASMIC C-TERMINAL
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; PubMed=11217851;
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Rodentia;
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SURFACE PROTEIN THAT MAY BE INVOLVED
LL ADHESION. MAY MEDIATE INTRACELLULAR
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Sciurognathi; Muridae;
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Query Match
Best Local 9
Matches 71
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                            GLMLHTGKSADYVNLALKNGAVSLVINLGSGAFEALVEPVNGKFNDNA - - -
                                                                                                                                                                                                                                                                                                                       GKVLMTG----GYLVLEKPNAGLVLSTN---ARFYAIVKPINEEVKPESWAWKWTDVKLTS
DNER
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MISSING (IN ISOFORM ALPHA
MISSING (IN ISOFORM ALPHA
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YJ9F_YEAST STANDARD; PRT; 1442 AA P47169; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Hypothetical 161.2 kDa protein in NMD5-HOM6 YJR137C OR J2126.

Eukaryota; Fungi;

Saccharomyces cerevisiae (Baker's

Ascomycota;

Saccharomycotina;

Saccharomycetes;

yeast) NMD5 - HOM6 _update)

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Best Local :
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARTTY: THE C-TERMINAL DOMAIN IS A 4FE-45/SIROHEME DOMAIN FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00397; SIRCHAEM.
PROSITE; PS00365; NIR_SIR; 1.
PROSITE; PS00365; NIR_SIR; 1.
Hypothetical protein; Oxidoreductase; Heme; Iron-sulfur; 4Fe-4S.
HYPOTHAL 1300 1300 IRON-SULFUR (4FE-4S) (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01077; NIR_SIR; 1.
Pfam; PF03460; NIR_SIR_ferr; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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NCBI_TaxID=4932;
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InterPro; IPR005117; Nir_sir_fer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                     7 LTLPQLLAQYSSSAPQNKV-FYTTSTKNSHSSF-KGLESVATDATHLLNNQDPLNTIKDQ
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                                                                   MVGAVKKWQMSDPEKARENWQNLSDA-----
                                                                                                         VVLTNIGNVNDYGNVINTVISNINKKEPDN----
                                                                                                                                                                                                   DLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSF------AQ
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                                                                                                                                                                                                                                                                 TGLGSS---
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                                                                                                                                                                                                                                                                                                                                                        LSKDILTTVFTDETTLVKSIHHLYSLPNKLPLVITVDLNLQDYSAIPALKDLSFPILISS
                                                                                                                                                                      -LEILPS-SVTKIAVLQG------VSKKSQSNEFQPFLLDFFGNFNELVSRNIEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
ETKLNDLSKLAKDHWD--VYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAR
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                                                                                                                                        -GLPLNEVIGTILKGKWDNKRTEFSLPPLMNLFLGEPGSGG---SSTPS
                                           ·····VVNLEDAYIKVLKQLFSSNLQILNQFSSETIEPSNPEFGFG
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IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107;
Pred. No. 8
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E34695088BA9FE94 CRC64;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X69894; CAAA9518.1; -.
Transferase; Glycosyltransferase.
SEQUENCE 698 AA; 77947 MW; 1704DF87A75CD835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The ADP-ribosyltransferases (gpAlt) of bacteriophages T2, T4, and T6: sequencing of the genes and comparison of their products."; Virology 203:294-298(1994).

-i- FUNCTION: COMPONENT OF THE PHAGE HEAD; ADP-RIBOSYLATES ONE OF TALPHA-SUBUNITS OF THE BACTERIAL RNA POLYMERASE.

-i- SUBCELLULAR LOCATION: THIS PROTEIN IS INJECTED FROM THE VIRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998
15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, T4-like viruses.
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NAD--protein ADP-ribosyltransferase (EC 2.4.2.-)
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                                   PLNEVIGTILKGKWDNKRTEF------SLPPLMNLFLGEPGSGGSSTPSMVGAVK 320
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P-DEVWGEITKNAWNAAKTKFLKRMIYSFSGIGAGPMIDITIARDGS--KYTPSQKRGIR
                                                                                                                                                                                PEVA------KTGLGSSAAMTTAV-----VAALLHY------LGVVDLSDPCKEG
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                                                                       ----VILNAIKNEPTTSIKCLEK-----
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                                                                                                                                              PATAPLIPEAEEMKLGINSLASKTKAAKIIAEGTANELHYDYKFFSKSEVNEVSEKIKD-
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Score 106;
Pred. No. 3
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                                                                       YAAAV--NQFFEEYKDNWLDKHNKTRKGQ
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
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16-OCT-2001 (Rel.
Mevalonate kinase
                                                                                                                                                                          InterPro; IPR001745; GHMPknse_ATP.
InterPro; IPR001459; Mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00959; MEVGALKINASE.
                                                                                                                                                                                                                                                                                                                                                                                    entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-i- CATALYTIC ACTIVITY: ATP + (R)-mevalonate
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                                                                              Transferase;
NP_BIND
                                                                                                                              TIGRFAMS; TIGR00549; mevalon_kin; 1 PROSITE; PS00627; GHMP_KINASES_ATP;
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SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYtoplasmic (Probable).
SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY.
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                                                                                                                                                               "Molecular evolution of vertebrate lactate dehydrogenas gene duplication.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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             entities requires a
                       use by non-profit institutions as long modified and this statement is not removed.
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TSOI S.C.-M., Li J.Y.,
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Cyprinidae; Danio.
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Eukaryota; Metazoa; Chordata; Craniata; Vert
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                               between
                                                                                                                                      -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) =
-!- PATHWAY: Anaerobic glycolysis; final step.
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SUBUNIT:
                                                                                                    SIMILARITY: BELONGS TO THE LDH FAMILY.
                                                                                                              SUBUNIT: Homotetramer (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By
                                                European Bioinformatics Institute.
                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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PROSITE; PR00064; LLDH; 1.
OXIDOREGUCTASE; NAD; Glycolysis; Multigene family.
OXIDOREGUCTASE; MULTIGENE FAMILY (BY SIMILARITY).
OXIDOREGUCTASE; MULTIGENE FAMILY (BY SIMILARITY).
OXIDOREGUCTASE; MULTIGENE FAMILY (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 HCLAQG--KVGSGFDVSCAVYGSQR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 GANSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 KIVADKDYSVTANSKVVVVVTAGARQQEGESRLNLVQRNVNIFKFIIPNIIKYSPNCILLV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GPTNKVTVVGVGMVGMAAAVSILLKDLTDELALVDVMEDKLKGE--AMDLQHGSLFLKTH 75
                                                                                                                                                                                                                                 DHWDVYLRVIKSC-SVLTSEKWVLHATEPINEAIIKELLEA-REAMLRIRILMRQMG--E 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 258
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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  155
149.5
147.5
142.5
                                                                                   372.5
178.5
178.5
                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                    is derived by analysis of the total score distribution
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length: 2000000000
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18.6
18.4
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                                                                                                                                                                                                                                                       Query
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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    IJ
                                       ABB77505
AAU15094
AAY72679
AAB18130
AAB185063
AAB60859
AAB99728
ABB49817
                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (without alignments)
1725.425 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908470
                                                                                                                                                                                                                               Description
Listeria monocytog
Mevalonate pathway
S. epidermidis ope
                                                                                                                                              Arabidopsis thalia
Protein encoded by
Candida albicans p
                                                             Streptomyces sp. C
                                                                                                       Pinus radiata phos
Enterococcus faeca
                                                                                 Mevalonate pathway
                                                                                                                                                                                                                                                                                                                                                          being printed,
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| Human protein SEQ | AAM79633 | 22 | 949 | 4.1 | | 45 |
|--------------------|----------|------|------|-----|--------|--------|
| | 231 | 22 | 949 | 4.1 | 105.5 | 44 |
| Human protein SEQ | AAM78649 | 22 | 931 | 4.1 | | 3 |
| | AAM79592 | 22 | 308 | 4.1 | 105.5 | 42 |
| | AAG31892 | 21 | 1087 | 4.1 | 106 | 41 |
| | AAG31893 | 21 | 1073 | 4.1 | 106 | 40 |
| | AAG31894 | 21 | 1056 | 4.1 | 106 | 39 |
| human | ABG15375 | 22 | 492 | 4.2 | 108 | 38 |
| | ABG06982 | 22 | 492 | 4.2 | 108 | 37 |
| | AAB01848 | 21 | 1477 | 4.2 | | 36 |
| Haemophilus high m | AAR63506 | 15 | 1477 | 4.2 | 108.5 | ω 5 |
| High molecular wei | AAR41728 | 14 | 1477 | 4.2 | • | 34 |
| yde-3- | AAR05738 | 11 | 369 | 4.2 | 109.5 | ω ω |
| Putative P. abyssi | AAB96178 | 22 | 338 | 4.3 | 112 | 32 |
| Rat corticosteroid | AAO14408 | 23 | 287 | 4.3 | 112 | 31 |
| Drosophila melanog | ABB71484 | 22 | 823 | 4.4 | 114 | 30 |
| Lactococcus lactis | ABB53952 | 23 | 816 | 5 | 115 | 29 |
| | AAY43633 | 21 | 432 | 5 | 115 | 28 |
| | AAM80073 | 22 | 723 | 5 | 115.5 | 27 |
| | AAM79089 | 22 | 952 | 5 | 116.5 | 26 |
| Human mevalonate k | AAR13720 | 12 | 396 | 4.5 | 117 | 25 |
| Arabidopsis thalia | AAG50072 | 21 | 456 | 4.8 | 123 | 24 |
| Arabidopsis thalia | AAG50073 | . 21 | 451 | 4.8 | 123 | 23 |
| Arabidopsis thalia | AAG50074 | 21 | 447 | 4.8 | 123 | 22 |
| Arabidopsis thalia | AAG50089 | 21 | 398 | 4.8 | 123 | 21 |
| Arabidopsis thalia | AAG51423 | 21 | 380 | 4.8 | 123 | 20 |
| | AAG51424 | 21 | 378 | 4.8 | 123 | 19 |
| Arabidopsis thalia | AAG50090 | 21 | 378 | 4.8 | 123 | 18 |
| | AAG12901 | 21 | 378 | | Ν | 17 |
| Mevalonate pathway | AAB60882 | 22 | 358 | | | 16 |
| Staphylococcus aur | 35 | 22 | 345 | • | ω 3 | 15 |
| Staphylococcus aur | AAU37273 | 22 | 358 | • | 35. | 14 |
| Mevalonate pathway | AAB60864 | 22 | 358 | ω | ω | 3 |
| Staphylococcus epi | ABP40510 | 23 | 362 | | 2 | 12 |
| Mevalonate pathway | AAB60883 | 22 | 358 | | 142.5 | 11 |

ALIGNMENTS

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PTTTX
                                                                                                                                                                                                                                                    RESULT 1
                              WPI; 2002-445360/48
N-PSDB; ABL60244.
                                                                                                                                                               growth regulator; enzyme.
                                                                                  22-NOV-2000; 2000DE-1057755.
                                                                                                                  23-MAY-2002.
                                                                                                                                  DE10057755-A1.
                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                       Thale cress; PMVK; phosphomevalonate kinase;
                                                                                                                                                                                      Arabidopsis thaliana PMVK SEQ ID NO
                                                                                                                                                                                                      29-JUL-2002
                                                                                                                                                                                                                      ABB77505;
                                                                                                                                                                                                                                     ABB77505 standard; Protein; 505 AA.
                                                    Meissner R,
                                                                                                  22-NOV-2000; 2000DE-1057755
                                                                  (FARB ) BAYER AG.
                                                    Lechelt-Kunze C;
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                        plant; herbicide;
```

New nucleic acid encoding plant phosphomevalonate kinase, useful for identifying modulators, potentially useful as herbicides and growth regulators $\dot{}$

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ARESULT 2
AAU15094
ID AAU1
XX AAU1
AC AAU1
XX
DT 04-D
XX
DE Prot
XX
Gene
KW Gene
XX
Gene
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Best Local S
Matches 505
                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid (I, ABL60244) that encodes a plant phosphomevalonate kinase (PMVK, ABB77505), excluding the known fully defined partial sequences ABL60245-ABL60247. Plant PMVK, (I), constructs and host cells that contain (I) are used to identify agent that bind to and/or modulate activity of PMVK, potentially useful as herbicides and growth regulators. (I) is also used for recombinant production of PMVK.
                                                                                                             Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                        WO200160975-A2
                                                                                                                                      Protein encoded by C.
              23-AUG-2001
                                                                   Candida albicans
                                                                                                                                                                     04-DEC-2001
                                                                                                                                                                                                                          AAU15094 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 100.0%;
Local Similarity 100.0%;
les 505; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL
                                                                                               replacement
                                                                                                             identification;
                                                                                                                                                                                                                                                                                                                                                                                                           VYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL
                                                                                                                                                                                                                                                                                                              HGVCLESGDPRTTCITSGVSSIHLE 505
                                                                                                                                                                                                                                                                                                                                                                  ESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVLALLVREDP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                      VYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTEFSLPPLMNL
                                                                                                                                                                                                                                                                                                HGVCLESGDPRTTCITSGVSSIHLE 505
                                                                                                                                                                                                                                                                                                                                                    ESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVLALLVREDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWD
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                                                                                                                                                                   (first
                                                                                               and
                                                                                                                                                                                                                          Protein;
                                                                                                                                                                  entry)
                                                                                               essential gene; conditional exp
                                                                                                                                      albicans essential gene CaYMR220W (ERG8).
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Pred. No. 1.7e-236;
; Mismatches 0;
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                                                                                               expression;
                                                                                                             GRACE;
                                                                                               pathogenic
; fungal inf
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identifial essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus funigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAUI5053-AAUI5113 represent proteins encoded by C. albican
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel methods for constructing strains useful for identification and validation of gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 43; Page 226-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2001;
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hes 144;
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                                                                                                                                                                                           FKHERCTLPHGIKLLMGDV-KGGSETPKLVSRVLQWKKEKPEESSVVYDQLNSANLQFMK
                                                                                                                                                                                                                                                                             CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK----GKWD
                                                                                                                                                                                                                                                                                                                                                                                         ---LEIIIYSDPGYHSQED------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPQLSR-ESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL 119 :||| :| | | :| | | :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAVVASAPGKYLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESMAWKWTDVKL
 LENPDYFHNVYWVDLEEQTEGVLEE
                                                                                MRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAW
                                                                                                                                                            KLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRIL
                                                                                                                                                                                                                                                                                                                                                                                                                         LQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNG-----AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSPQFANGEWEYHISSN--TEKPKEVQSRINPFLEATIFIVLAYIQPTEAFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSKAFSAPGKAFLAGGYLVLEPIYDAYVTALSSRMHAVITPKGTSLKE-----SRIKI 53
                                SS----
                                                              LQALTQKSEVPIEPDVQTQLLDRCQEIPGCVGGVVPGAGGYDAIAVLVLEHQVGNFKQKT
                                                                                                                              ELREMREKYDSDPETYIKELD-----
                                                                                                                                                                                                                                                           CYAQKKIGSGFDVATAIYGSIVYRRFQPALINDVFQVLESDP--EKFPTELKKLIASNWE
                                                                                                                                                                                                                                                                                                                           AITEVEKTGLGSSAGLVSVVATSLLSHFIPNVIS--
                                                                                                                                                                                                                                                                                                                                                       SKPEVAKTGLGSSAAMTTAVVAALL-HYL-GVVDLSDPCKEGKFGCSDLDVIHMIAQTSH 230
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                                                                                                                                                                                                                           NKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 28.9
44; Conservative
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                              HNVLALLVREDPHGVCLE
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28.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
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Pred. No. 1.4e-36;
8; Mismatches 183;
 424
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                                                                                                                                                                                                                                                                                                                                                                                         -TETKTSSNGEKTFLYHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 100;
                                                                                                                                                                                                                                                                                                                            TNKDILHNVAQIAH
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Best Local S
Matches 143
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                                                                                                                                                                                                                                                                                                                         The present sequence is phosphomevalonate kinase (PMK; ERG8) protein from Candida albicans. The ERG8 protein is useful in an assay for identifying compounds that inhibit phosphomevalonate kinase (PMK) activity. These inhibitors are useful as anti-fungal agents. The ERG8 DNA and protein are also useful as reagents for diagnosing C. albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides and polynucleotides (ERG8) from Candida albicans useful in assays for identifying inhibitors of phosphomevalonate activity and as reagents for diagnosing C. albicans infection -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosamond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
                                                                                                                                                                                                                                                                                                                   infection
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                                                                                                                                                                                                                   1 MAVVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKL
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DB; AAD02791, AAD02792
                                                                                                                                         SSPQFANGEWEYHISSN--TEKPREVQSRINPFLEATIFIVLAYIQPTEAFD-----
                                                                                                                                                                    TSPQLSR-ESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLL
                                                                                                                                                                                            MSKAFSAPGKAFLAGGYLVLEPIYDAYVTALSSRMHAVITPKGTSLKE------SRIKI
CYAQKKIGSGFDVATAIYGLIVYRRFQPALINDVFQVLESDP--EKFPTELKKLIESNWE
                       CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK----GKWD
                                                                       SKPEVAKTGLGSSAAMTTAVVAALL-HYL-GVVDLSDPCKEGKFGCSDLDVIHMIAQTSH
                                                 AITEVEKTGLGSSAGLVSVVATSLLSHFIPNVIS-
                                                                                                ---LEITIYSDPGYHSQED----
                                                                                                                     LQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNG-----AN
                                                                                                                                                                                                                                                      Similarity
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ASTRAZENECA UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JDC,
                                                                                                                                                                                                                                                                                           432
                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase; PMK; ERG8; anti-fungal agent; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                      18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                  29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432
                                                                                                                                                                                                                                                     Score 475; DB 22;
Pred. No. 4.3e-36;
                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                           184;
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                                                                                               -TETKTSSNGEKTFLYHSR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERG8) protein
                                                                                                                                                                                                                                                                Length 432;
                                                                                                                                                                                                                                          Indels
                                                 -TNKDILHNVAQIAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shown
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 243
                         286
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PR

The present invention

polypeptides involved

describes plant polynucleotides encoding in the production and modification of isoprenoids, steroid compounds. The polynucleotides are used

such as terpenoid and

Claim 26; Page 159; 164pp; English.

applications, manipulating isoprenoid pathways or isoprenoid composition may, for example, affect plant development, pest resistance, and the value of extractives (e.g. pinene and myrcene). The ubiquitous and

varied roles of isoprenoids make the polynucleotides attractive

e e

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targets

for biotechnical applications in

in genome mapping, in physical mapping and in positional cloning of genes. The polynucleotides and polypeptides are useful in forestry and agriculture for manipulation of isoprencia metabolism, in medicine for therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms and in fermentation and chemical processing industries involving isoprenoids. In plant

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AAB18130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant; metabbolism; isoprenoid biosynthetic pathway; terpenoid; steroid; genome mapping; physical mapping; positional cloning; forestry; agriculture; medicine; fermentation; plant development; pest resistance;
agriculture for manipulation of isoprenoid metabolism
                                     New plant polynucleotides encoding polypeptides involved in production and modification of isoprenoids, useful in forest
                                                                                              N-PSDB; AAA69566
                                                                                                                                                          Havukkala IJ
                                                                                                                                                                                                                                                       17-DEC-1998;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                  16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                          22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                               WO200036081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pinene; myrcene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18130;
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                                                                                                                                                                                           (GENE-) GENESIS F
(FLET-) FLETCHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphomevalonate kinase protein SEQ ID
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99US-0146441.
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R CHALLENGE FORE
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RESULT 5
AAU35063
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AC AAU3
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AC AAU3
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KW AAT1
KW AAT1
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                                                                                         The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The attisense nucleic acids can also be used
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23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; | antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA69690 and AAB18004 to radiata polynucleotides a present invention.
                                                                                                                                                                                                                                                                                                                                                                           antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU35063 standard; Protein;
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27-NOV-2000;
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               identify proteins used in proliferation, to express these proteins, d to obtain antibodies capable of binding to the expressed proteins e proteins can be used to screen compounds in rational drug discover
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a wide variety of organisms. The present sequence rep
essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form
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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an isolated mevalonate pathway derived from a bacterium from clade of Class II of the phylogenetic tree referred to in the specification. The inventioused for treatment of disease related to bacterial infection, econjunctivitis, pneumonia, bacteremia and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown JR,
Wilding EI
                                                                 Streptomyces sp. CL190; mevalonate pathway; actinomycete; carcisoprenoid compound; osteopathic; cytostatic; ubiquitone; vita carotenoid; heart disease; osteoporosis; cancer; drug; health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
             WO200142476-A1
                                         Streptomyces sp.
                                                                                                                                Streptomyces
                                                                                                                                                           10-SEP-2001
                                                                                                                                                                                          AAB99728;
                                                                                                                                                                                                                       AAB99728 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
                                                                                                                                                                                                                                                                                             TEALKNLCDLAESYTGA--AKSSGAGGGDCGIVIFRQKSGILPLMTAWEKDGITPL
                                                                                                                                                                                                                                                                                                                        PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVLAL 474
                                                                                                                                                                                                                                                                                                                                                                                 DVYLRVIKSCSVLTSEKWYLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE 419
                                                                                                                                                                                                                                                                                                                                                                                                                                           LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDIAASCYGG--WIAFSTFDHDWVNQKVT----TETLTDLLAMDWPELMIFPLKVPKQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT-EFSLPPLMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSGAVTVGTVKALNIFYDLGL------ENEEIFKLSALAHLAVQGN-GSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-
                                                                                                                                                                                                                                                                                                                                                                                                               LLIGWTGS-PASTSDLVDRV----HQSKEEKQAAYEQFLMKSRLCVETMINGFN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
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106; Conservat
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A
                                                                                                                             CL190 mevalonate pathway orfC
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Pred. No. 5.6e-08;
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                                                                    vitamin K
alth food.
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Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences encoding them have cardiant, osteopathic and cytostatic activities. The genes are applicable in producing e.g. ubiquitone, vitamin K2 and carotenoids which can be used in the treatment of heart diseases, osteoporosis and cancer in drugs and health foods. The present sequence represents the orfC protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence given in AAH44043 represents a DNA sequence isolated from Streptomyces sp. CL190, containing a 6798 base pairs (Sl), which encode the whole enzyme necessary for functioning the mevalonate pathway. The sequence encodes protein sequences, designated orfA to E and hmgr, which are used in the mevalonate pathway. The proteins and polynocleotide
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(KUZU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetes-originated genes of enzymes participating in mevalonate pathway, applicable in producing e.g. ubiquitone, vitamin K2 and carctenoids for treatment of heart diseases, osteoporosis and cancer ideng and health food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                    CLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT
VRQRWETAGVLPL
                           --QAWSSHNVLAL
                                                                                                                                                                                                                                                                                                         NSKPEVAKTGLGSSAAMTTAVVAALLHYLGV-VDLSDPCKEGKFGCSDLDVIHMIAQTSH 230
                                                                         LMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVP-GAGGFDAIFAITLGDSGTKLT-
                                                                                                                                            TKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRI
                                                                                                                                                                         R-RLPAPKGLTLEVGWTGEP---
                                                                                                                                                                                                      EFSLPPLMNLFL----GEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELE
                                                                                                                                                                                                                                                                                                                                                                                                                                         AWKWTDVKLTSPOLSRESMYKLSLNHLTLOSVSASDSRNPFVEHAIQYAIAAAHLATEKD
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KUZUYAMA
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                                                      -LDDEVGLGIFTPKLTALCD----AAEAVGGAAKPSGAGGGDCGIALLDAEASRDITH
                                                                                                                                                                                                                                   --PKGSGGDLAASTWGG--WIAYQAPDRAF----VLDLARRVGVDRTLKAPWPGHSV
                                                                                                                                                                                                                                                                                             --- RKFGLGSSGAVTVATVAAVAAFCGLELSTDERFRLAMLATAELD-
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                                                                                                                -TTDCVRSAVTALESGD--DTSLLHEIRRARQELAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 155; DB 2:
Pred. No. 1e-05;
68; Mismatches 1:
                                                                                                                                                                         -ASTASLVS
                                                                                                                                                                                                                                                                                                                                                     -SAIETVGRLLGERGQKVPALTLSVSSRLHEDG--
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172; 22;

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Matches 99
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Chakraborty T, Doma...
Perez-Diaz J, Baquero F
Perez-Diaz De Pablos P
                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dussurget O, Cheton
Daniels J, Goebel O
Dominguez-Bernal G,
                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                     encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytopens and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2001;
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                                                                                                                                                                                                            monocytogenes and related organisms.
                                                                                                                                                                                                                         sequence and proteins encoded by it are useful in pharmaceutical vaccines compositions for the treatment or prevention of infecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                        polymorphisms and other genomes.
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                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                         modulate L. monocytogenes-related diseases.
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PGKLYVAGEYAVVESGHTAILTAVN-RYITLTLEDSERNELWIPHYENPVSWPVGGELKP
                               PGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVK-----
                                                                             Similarity
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                                                        Score 149.5; DB 23;
Pred. No. 3.1e-05;
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                              -----PINEEVKP 48
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                                                                                            Length 359;
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Cossart P;
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                                                                                                                                       Brown JR, (
Wilding EI;
The present invention relates to an isolated mevalonate pathway gene derived from a bacterium from clade of Class II of the phylogenetic tree referred to in the specification. The invention may used for treatment of disease related to bacterial infection, e.g.
                                                                               New isolated mevalonate bacterium is useful for
                                                                                                                  WPI; 2001-071392/08
                                                                                                                                                                                                            22-JUN-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                 Enterococcus faecium
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                                                           Claim
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                                                                                                                                                                                                                                                                                                                                       Mevalonate pathway;
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                                                        20; Page 33;
                                                                                                                                                                          SMITHKLINE BEECHAM SMITHKLINE BEECHAM
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99US-0146682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis open reading
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WPI; 2001-316495/33
                                                      Kimmerly WJ
                                                                                                                                                               09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                  epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SR1 strain; infection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frame protein sequence SEQ ID NO:918
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Pred. No. 4.9e-05;
""smatches 171;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AA681454 to AA683120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polypucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH55098 represent oligonucleotide sequences and primers which are use in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 447 no sequences are present for SEQ ID NO:4455 to 4464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 KTLHYEPVKFDRNEDRIEISDVQAAKQ-----LKYVVTAIEV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
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                                                                                                                                      GDFLDQSHAC
                                                                                                                                                                                                                     VLIGWTGSPASS-PHLVSEVKRLK-SDP----
                                                                                                                                                                                                                                                                                                DIAVSVYSGWLAYSTFDHDWVK-QQMEETS----VNDVLEKNWPGLHIEPLQAPENME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQVKAPGKLYIAGEYAVTEPGYKSILIAVNRFVTATIEASNK------VEGSIHS
                                                            ETDKLKKLCDVGEKHGGA - - SKTSGAGG
                                                                                               EPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVL 472
                                                                                                                                                                              DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRI-RILMRQMGEAASVPI 418
                                                                                                                                                                                                                                                                                                                                                                                 LGSSAAVLVSVVKALNEFYG-LELSNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacids encoding polypeptides from Staphylococcus epidermidis, for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 19.8
94; Conservative
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Pred. No. 0.00014;
2; Mismatches 167
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                                                            -GDCGITIINKVIDKNII 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                               phylogenetic tree referred to in the specification. The invention may used for treatment of disease related to bacterial infection, e.g. conjunctivitis, pneumonia, bacteremia and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to an isolated mevalonate pathway derived from a bacterium from clade of Class II of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1999;
02-AUG-1999;
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                                                                  DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRI-RILMRQMGEAASVPI
                                                                                             VLIGWTGSPASS-PHLVSEVKRLK-SDP
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 ETDKLKKLCDVGEKHGGA--SKTSGAGG
                     EPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNVL
                                               GDFLDQSHAC
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SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwynn M,
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19.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus antibacterial;
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08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screen for compounds able to interfere with the S. epidermidis life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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DVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMN
                                                                                                          LGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGF
                                                                                                                                                                                                                    GLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKFEVAKTG
                                                                                                                                                                                                                                                                         KTLHYEPVKFDRNEDRIEISDVQAAKQ-----LKYVVTAIEV----
                                                                                                                                                                                                                                                                                                                           PQLSRESM-YKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQ 121
                                                                                                                                                                                                                                                                                                                                                                                      IQVKAPGKLYIAGEYAVTEPGYKSILIAVNRFVTATIEASNK
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94; Conservative
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97US-064964P
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19.8%;
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Best Local :
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                                                                                                                                                                                                                                                                          The present invention relates to an isolated mevalonate pathway gene derived from a bacterium from 60 Class II of the phylogenetic tree referred to in the specification. The invention may used for treatment of disease related to bacterial infection, e.g. conjunctivitis, pneumonia, bacteremia and meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilding
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                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated bacterium is
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02-AUG-1999;
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                                                                                                                                      VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
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                                                                                                      IQVKAPGKLYIAGEYAVTE-PGYKSVLIALDRE--VTATIEEATQ-----YKGT-----
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   LQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAK 179
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Pred. No. 0.00054;
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27-NOV-2000;
22-DEC-2000;
                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
                                                                                                                                                                                                                        WPI; 2001-611495/70.
N-PSDB; AAS55132.
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23-MAY-2000;
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invention is also useful
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
Example 3; Seq ID No 12866; 511pp; English.
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                                                                                                                                                                                                                          ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prokaryotic cellular
                                                                                                                                                                                                                                                              2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial;
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                                                                                                                                  Staphylococcus
                                                                                                                                                                             antibiotic; antibacterial;
                                                                                                                                                                                                    Antisense;
                                                                                                                                                                                                                                           Staphylococcus aureus cellular proliferation protein #634
                                                                                                                                                                                                                                                                                         14-FEB-2002
                                                                                                                                                                                                                                                                                                                                    AAU34358
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    21-MAR-2001; 2001WO-US09180
                                             27-SEP-2001.
                                                                                      WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                           AAU34358 standard; Protein; 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
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                                                                                                                                                                             design
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for antibiotic development. The antisense nucleic acids can also be us to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discover
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Yamamoto RT,
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16-FEB-2001;
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Search completed: April 26, 2003, 12:55:05 Job time: 42 secs

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US-09-134-001C-5355
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APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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Indels

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NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/475,577
FILING DATE: 06-FEB-1990
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TITLE OF INVENTION:
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                                                   Sequence 8, Application Patent No. 6284506 GENERAL INFORMATION:
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APPLICANT: HOSHINO, Tatsuo
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 396
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                                                                                                                                                                                   KQALTSCGFD-----CLE----TSIGAPGVSIH
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                                                                                                                                                                                                                                                                                                                                -----APAPEQYLVLEELIDMNQHHLN-----
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20.2%;
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; ORGANISM: Phaffia rhodozyma
US-09-306-595C-8
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                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08038682 Patent No. 5549897
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                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ISOPRENOID PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                  TITLE OF INVENTION: HITTITLE OF INVENTION: OF NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                      STREET: 2001 Jef.
STREET: Bldg. 1
STRY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 NSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHC
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                                                                      COUNTRY: U.S.A. ZIP: 22202-0286
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Local Similarity 21.6%;
ses 103; Conservative 6
                   COMPUTER:
OPERATING
                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          KPFELRTKLTGAGGGGCAVTLVPDDFSTETLQALMETLVQSSFAPYIARVGGSGVGF
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IBM PC
SYSTEM:
                                                                                                                                                          2001 Jefferson
                                                                                                                                                                                                                                                                          BARENKAMP, STEPHEN ST. GEME III, JOSEF
                                                                                                                                                                                 Shoemaker and Mattare,
PC-DOS/MS-DOS
                                                                                                                                                                                                                       OF NON-TYPEABLE
8
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HIGH MOLECULAR WEIGHT SURFACE
                                                                                                                                                                Davis
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Pred. No. 0.0032;
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, 1203 Crystal Plaza
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                                                                                                                                                                                   Sequence 4, Application US/08302832 Patent No. 5603938
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                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Barenk
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INFORMATION FOR SEQ
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                  TITLE OF INVENTION:
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                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                  TVNSSINIGSNSHLILHS 524
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                                                                                                                                                                                                                                                                                                                                                                                  TPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLND--LSKLAKDHWDV-----YL 363
                                                                                                                                                                                                                                                                                                                                                                                                                  AKTGGFVETSGHDLFIKDNAIVDA----KEWLLDFDNVSINAEDPLFNNTGINDEFPTGTG 468
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Virginia
                                    Bldg.
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                                                                                                                                                 Barenkamp, Stephen J
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                                           Shoemaker and Mattare, Ltd.
01 Jefferson Davis Hwy., 1203 Crystal Plaza
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of No. 5603938-Typeable
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Pred. No. 0.13;
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
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22202-0286
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Sequence 4, Application US/08530198 Patent No. 5869065

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Best Local Similarity 20.3%;
Matches 89; Conservative
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STRANDEDNESS: si
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JW
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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HIGH MOLECULAR WEIGHT SURFACE PROTEINS
OF NON-TYPEABLE HAEMOPHILUS
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Best Local Similarity 20.3
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2001 Jef.
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                   163 FNAAESNGA-NSKPEVAKTG----LGSSAAMTTAVVAALL-----HYLGVVDLSDPCKE 211
                                                                                                                                                        199 NHGLITYGKDGSYNLIGGKYKNEGYISYNGGSISLLAGQKITISDIINP----TITYSIA 254
                                                                                                                                                                                                                                        139 ILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                              11 VLMTGGYLVLEKPNA-----GLVLSTNARFYAIVKPINEEVKPESWAWKWT------
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CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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EGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLG----GDERGE
                                                                             ----APENEAVNLGDIFAKGGNINVRAA----TIRNQGKLSADSVSKDKSGNIV--LSAK 304
                                                                                                               AAHLATEKDKESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASIT 162
                                                                                                                                                                                                ------DVKLTSPQLSRESMYKL---SLNHLTLQSVSASDSRNPFVEHAIQYAIA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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High Molecular Weight Surface Proteins
of No. 5876733-Typeable Haemophilus
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                               Length 1477;
                                                                                                                                                                                                                                                                                                                        Gaps
360
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21;

| Query Match 4.2%; Score 108.5; DB 2; Length 1477; Best Local Similarity 20.3%; Pred. no. 0.13; Matches 89; Conservative 68; Mismatches 162; Indels 119; Gaps 21; Matches 100; Matches 100; Gaps 21; Matches 100; Conservative 100; Mismatches 162; Indels 119; Gaps 21; Matches 100; Conservative 100; Mismatches 162; Indels 119; Gaps 21; Matches 100; Conservative 100; Mismatches 100; Misma | ; LENGTH: 1477 amino acids ; TYPE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear US-08-728-470-4 | 10N: . | ; APPLICATION NUMBER: GB 9205704.1 ; FILING DATE: 16-MAR-1992 ; ATTORNEY_AGENT INFORMATION: ; NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22,651 ; REFERENCE_CONCET NUMBER: 1038-633 | CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993 PRIOR APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: | COUNTRY: U.S.A. 21P: 2202-0266 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/728,470 FILING DATE: | Patent No. 5928651 Patent No. 5928651 GENERAL INFORMATION: APPLICANT: Barenkamp, Stephen J FITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd. STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bidg. 1 CITY: Arlington STATE: Virginia | 507 TVNSSINIGSNSHLII SULT 8 -08-728-470-4 | Qy 212 GKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV 266 |
|--|---|---------|--|---|---|--|---|--|
| 10N: | | U Z U O | COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/617,697 FILME DATE: US/08/617,697 | | 617 ence nt l ERAI PPL ITLI ITLI UMBI ORRI | Db 412 AKTGGFVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTG 468 Qy 312 TPSMVGAVKKWOMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWDVYL 363 Db 469EASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKL 506 QY 364 RVIKSCSVLTSEKWVLHA 381 | 212 GKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQV | Db 139 ILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNETFEQTKDKALAEIV 198 Qy 57DVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIA 102 |

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US-08-719-641-4
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Patent No. 621814
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                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 16-SEP-1994
                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                    FILING DATE
                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                  ZIP: 22202-0286
   APPLICATION
                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKITISDIINP----TITYSIA
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                                                                                                                                                                                                                                                                Virginia
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                                                                                                                                                                                                                                                                                                            2001 Jefferson Davis Hwy.,
                                                                                                                                                                                                                                                                                                                                                              Barenkamp, Stepnen J
VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 6218141-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DVKLTSPQLSRESMYKL---SLNHLTLQSVSASDSRNPFVEHAIQYAIA 102
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                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           Shoemaker and Mattare, Ltd.
101 Jefferson Davis Hwy., 1203 Crystal Plaza
   NUMBER
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                                                 US 08/302,832
US PCT/US93/02166
                                                                                                                 US/08/719,641
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Pred. No. 0.13;
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                                                                                                                                                  Version #1.30
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                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                        Sequence 71, Appli
Patent No. 6432669
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                                                                                                 TITLE OF INVENTION: Protective Recombinant Haemophilus TITLE OF INVENTION: Molecular Weight Proteins
                                                 CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 1998-12-08
                                                                                     FILE REFERENCE: 1038-861 MIS:jb
                                                                                                                                   APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel
                 EARLIER FILING DATE: 1998-10-07
                               EARLIER APPLICATION NUMBER: 09/167,568
                                                                                                                                                                      APPLICANT: Loosmore, Sheena
NUMBER
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TELEPHONE: (703) 415-0810
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                                                                                                                                                                                                                                                                                                          507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Berkstresser, Jerry REGISTRATION NUMBER: 22,69
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; TYPE: PRT ; ORGANISM: Haemophilus influenzae US-09-206-942-71

SEQ ID

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                                                                                                                                              SEQ ID NO 4
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Best Local Similarity
                                   Query Match
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   Matches
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                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-
                                                                                      LENGTH: 441
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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y Match 4:0%; Score 104.5; DE
Local Similarity 22.3%; Pred. No. 0.042;
nes 87; Conservative 45; Mismatches 1
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351 VLQQDAHGSVTITGQPMTFPPEALWVTVGLS 381
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                                                                           FWQDGQGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGT--
                                                                                                             --MSAEGVLLAG-----VPGAGGFD--AIFAITLGDSGTKLTQAWSSHNVLALLVR-- 477
                                                                                                                                                                                                                               Q------LTDTKQLVHSFTEGRDQGSAYANRTALFPDLLAQGNASLRLQRVRVAD
                                                                                                                                                                                                                                                                                                          ITPQRSPTGAVEVQVPEDPVVALVG----TDATLHCSFSPEPGFSLTQLNLI------W 192
                                                                                                                                                                                                                                                                                                                                                 STP--SMVGAVKKWQMSDPEKARENWQNLSDANLELE-----TKLNDLSKLAKDHW 359
                                                                                                                                                                                                                                                                                                                                                                                          G-QGVPLT---GNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSSVT 143
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                                                                                                                                                      EGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEV 301
                                    ---EDPHGVCLESGDPRT---
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                                    --TCITSGVS 500
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RESULT 13
US-08-445-135-2
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                                                                                            TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     APPLICATION NUMBER: US 01 FILING DATE: 12-NOV-1993 ATTORNEY AGENT INFORMATION:
   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                          TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                         REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                              TOPOLOGY:
                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                               amino acid
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                                                                                                                                                                                                   Israelsen, Ned A.
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                                                                          770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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; ORGANISM: Homo sapiens US-09-651-200-6
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09651200 Patent No. 6429303
                                                                       SOFTWARE:
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0
                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-1
                                                                                                                                                                                                                                          FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/69
CURRENT FILING DATE: 2000-08-30
                                                                                                                                                                                                                                                                                              APPLICANT: Green et al TITLE OF INVENTION: Polynucleotides Encoding Members of the Human TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and TITLE OF INVENTION: Polypeptides Encoded Thereby
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-09-03
                                    TYPE: PRT
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                                                    ENGTH: 534
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19.1%; Pred. No. 0.
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                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism: ; OTHER INFORMATION: mz5020.protein from Figure 4. US-09-651-200-24
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SOFTWARE: Patentin V
SEQ ID NO 24
                                                                                   Query Match
Best Local :
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Best Local
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PRIOR FILING DATE: 1999-(
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-
                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651
CURRENT FILING DATE: 2000-08-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                             LENGTH: 534
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                                183 GSSAAMTTAVVAALLHY-----LGVVDLSDPCKEGKFGC------SDLDVIHMI 2
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GSAYANRTALFPDLLAQGNASLRLQRVRVAD----EGSFTCFVSIRDFGSAAVSLQVAAPY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FD--AIFAITLGDSGTKLTQAWSSHNVLALLVR-----EDPHGVCLESGDPRT----TC
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                                                                   Similarity
97; Conserv
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97; Conserv
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                                                                 Score 101.5; DI
Pred. No. 0.12;
48; Mismatches
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Pred. No. 0.12;

    YSCLVRNPVLQQDAHGSVTITGQPMTFPPEALW 468

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                                                                     Indels 145;
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| Qy | 226 AQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK 282 | |
|----|--|---------|
| ф | 143 SKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDG-QGVPLTGNVTT 192 | |
| Qγ | GSGGSSTPSMVG | - |
| Ъ | 193 SQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSSVTITPQRSPTGAVEVQVP 252 | .5 |
| Qy | 325 SDPEKARENWONLSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHA-TE 383 | |
| рb | 253 EDPVVALVGTDATLRCSFSPEPGFSLAQLULIWQLTDTKQLVHSFTE 299 | v |
| Qγ | AMLRIR | _ |
| B | 300 GRDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAP 359 | v |
| Qy | 415SVPIEPESQTQLLDSTWSAEGVLLAGVPGAGG 446 | |
| Db | 360 YSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGL 419 | v |
| Qy | - | |
| ₽ | 420 EDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEALW 468 | w |
| δĀ | 495 ITSGVS 500 | |
| В | 469 VTVGLS 474 | |

Search completed: April 26, 2003, 12:57:54 Job time : 22 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seg length: 2000000000
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2581
1 MAVVASAPGKVLMT
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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and is score greater than derived by analysis of the total score distribution. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,

SUMMARIES

| Result No. | Score | Query Match | Query Match Length DB | 80 | ID · | Description |
|---------------|-------|----------------|--------------------------|----|---------------------|-------------------|
| 1 | 2581 | 100.0 | 505 | 10 | US-09-988-863A-2 | Sequence 2, Appli |
| N | 575 | 22.3 | 179 | 10 | US-09-909-745-22 | 22 |
| ω | 453.5 | 17.6 | 451 | 10 | US-09-909-745-24 | 24 |
| 4 | 216 | 8.4 | . 67 | 10 | US-09-909-745-20 | 20 |
| σ | 204 | 7.9 | 54 | 10 | US-09-909-745-16 | Sequence 16, Appl |
| 6 | 204 | 7.9 | 54 | 10 | US-09-909-745-18 | 18 |
| 7 | 178.5 | 6.9 | 368 | 10 | US-09-815-242-10656 | 106 |
| æ | 135.5 | 5.2 | 358 | 10 | US-09-815-242-12866 | |
| 9 | 133.5 | 5.2 | 345 | 10 | US-09-815-242-5854 | |
| 10 | 126 | 4.9 | 386 | 10 | US-09-909-745-26 | Sequence 26, Appl |
| 11 | 123 | 4.8 | 378 | 10 | US-09-909-745-23 | Sequence 23, Appl |
| 12 | 115 | 4.5 | 432 | 9 | US-09-925-388-8 | Sequence 8, Appli |
| 13 | 108.5 | 4.2 | 1477 | ဖ | US-10-092-880-4 | Sequence 4, Appli |
| 14 | 101.5 | 3.9 | 534 | Q | US-10-077-023-7 | Sequence 7, Appli |
| 15 | 101.5 | 3.9 | 534 | 10 | US-09-875-338-7 | |
| 16 | 101 | 3.9 | 1025 | œ | US-08-910-386A-7 | Sequence 7, Appli |
| 17 | 100 | 3.9 | 335 | 10 | US-09-815-242-13670 | Sequence 13670, A |
| 18 | 100 | 3.9 | 698 | 9 | US-10-077-023-9 | Sequence 9, Appli |
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 88 | 88.5 | 88.5 | 89 | 89 | 89.5 | 90.5 | 90.5 | 90.5 | 91 | 91 | 91 | 91 | 91.5 | 92 | 92 | 92.5 | 92.5 | 92.5 | 93.5 | 94 | 95 | 95.5 | 96 | 96 | 97 |
| 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.5 | 3.5 | | | | | | | | | | | | | | | | | 3.7 | 3.7 | ω œ |
| 633 | 2344 | 551 | 3313 | 1173 | 794 | 7968 | 1165 | 551 | 1386 | 730 | 714 | 679 | 1176 | 532 | 385 | 948 | 640 | 514 | 806 | 387 | 492 | 1599 | 854 | 657 | 863 |
| 10 | 10 | 10 | 10 | 9 | 10 | 9 | 10 | 9 | 10 | 10 | 9 | 10 | 9 | 9 | 10 | 9 | 10 | 9 | 12 | 10 | 9 | 9 | 9 | 10 | O. |
| US-09-815-242-13318 | US-09-815-242-12713 | US-09-897-214-8 | US-09-737-149-29 | US-10-135-322-19 | US-09-815-242-11829 | US-10-077-130-5 | US-09-815-242:10744 | US-10-078-770-158 | US-09-866-582-38 | US-09-815-242-12489 | US-10-098-807-2 | US-09-815-242-5407 | US-09-918-508-2 | US-09-966-614-2 | US-09-853-918-37 | US-10-267-311-21 | US-09-918-951-4 | US-09-738-626-5869 | US-10-003-405-2 | US-09-789-561-156 | US-09-738-626-5963 | US-10-092-880-9 | US-09-770-107-2 | US-09-815-242-13436 | US-U9-946-239-11 |
| Sequence 13318, A | Sequence 12713, A | Sequence 8, Appli | Sequence 29, Appl | Sequence 19, Appl | Sequence 11829, A | Sequence 5, Appli | Sequence 10744, A | Sequence 158, App | Sequence 38, Appl | Sequence 12489, A | Sequence 2, Appli | Sequence 5407, Ap | Sequence 2, Appli | Sequence 2, Appli | Sequence 37, Appl | Sequence 21, Appl | Sequence 4, Appli | Sequence 5869, Ap | Sequence 2, Appli | Sequence 156, App | Sequence 5963, Ap | Sequence 9, Appli | Sequence 2, Appli | Sequence 13436, A | Sequence II, Appr |

ALIGNMENTS

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; SEQ ID NO 2;
LENGTH: 505;
; TYPE: PRT;
; ORGANISM: Arabidopsis thaliana
US-09-988-863A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09988863A Patent No. US20020123427A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 505; Conserv
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Plant phosphomevalonate kinases FILE REFERENCE: Le A 35 018 CURRENT APPLICATION NUMBER: US/09/988,863A CURRENT FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bayer AG
181 GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
                                                                                          181 GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
                                                                                                                                                                                                                61 TSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Falco, S. Carl

APPLICANT: Falco, S. Carl

APPLICANT: Famodu, Omolayo O.

TITLE OF INVENTION: Squalene Synthesis Enzymes

FILE REFERENCE: BB1112 US CIP

CURRENT APPLICATION NUMBER: US/09/909,745

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: 60/107,241

PRIOR APPLICATION NUMBER: 60/107,241

PRIOR APPLICATION NUMBER: 60/107,241

PRIOR FILING DATE: 1998-11-05

PRIOR FILING DATE: 1998-11-05
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                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                      Sequence 24, Application US/09909745
Patent No. US20020119546A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                        CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
                                                                                                 APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
NUMBER OF
             PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Office 97
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nes 111; Conserv
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                                                                                                                                                                                                                                                                                                                  SCSRLTCSKWTEVATNOHOELIVRSLLAARDAFLEIRLHMREMGIAAGVPIEPESQTQLL 120
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 SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                22.3%; Score 575; DB 10; 62.0%; Pred. No. 1.8e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 179;
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; ORGANISM: Oryza sativa
US-09-909-745-20
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                                                                                                                                SOFTWARE: Microsoft Office
SEQ ID NO 20
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09909745 Patent No. US20020119546A1
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Matches 155;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR EPILING DATE: 1008-11-05
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Famodu, Omolayo O. TITLE OF INVENTION: Squalene SFILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Falco, S. APPLICANT: Famodu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 451
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 LRAQTANDKRFSKVQWLDVTQADWGVRKEK-DPET 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 EEDWNITIKSNHLPSGLTLWMGDI-KNGSETVKLVQKVKNWYDSHMPESLKIYTELDHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 QAQGKIGSGFDVAAAAYGSIRYRRFPPALIS-----NLP---DIGSATYGSKLAHLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 LAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 HRIEEVPKTGLGSSAGLVTVLTTALASFF-VSDLENNVDKYR-----EVIHNLAQVAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 NSKPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 KPNMDDYCNRNLFVIDIFSDD--AYHSQEDS-----VTEHRG------NRRLSFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 KESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 MLRIRILMROMGEAASVPIEPESOTOLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 ---WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDAN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 TDVKLTSPQLSRESMYKLSLNHLTLQS----VSASDSRNPFVEHAIQYAIAAAHLATEKD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINE-----EVKPESWAWK---W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 SAPGKALLAGGYLVLDTKYEAFVVGLSARMHAVAHPYGSLQGSDKFEVRVKSKQFKDGEW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKLTQAWSSH--NVLALLVREDPHGVCLESGDPRT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VATIRRSFRKITKESGADIEPPVQTSLLDDCQTLKGVLTCLIPGAGGYDAIAVITKQDVD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SREMDGLSKLDRLHETHDDYSDQIFESLERNDCTCQKY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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8.4%;
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                                                                                                                                                                                                                                                                                                                                                                                            Synthesis Enzymes
Score
Pred.
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216; DB 10;
No. 8.5e-12;
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                     Length 67;
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Matches

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; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
US-09-909-745-18
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; ORGANISM: Zea mays
US-09-909-745-16
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US-09-909-745-16
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Best Local Similarity 74.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application (Patent No. US20020119546A)
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                                                                                                            Query Match
                                                                                                                                                                                                                        SEQ ID NO 18
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Patent No. US20020119546A1
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                                           PRIOR FILING DATE: 19
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
                                                                                                                                                                                                                                           SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
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ITLE OF INVENTION: Squalene Synthesis Enzymes
ILE REFERENCE: BB1112 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 REAMLRIRILMROMGEAASVPIEPESOTOLLDSTMSAEGVLLAGVPGAGGFDAI
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                 397 REAMLRIRILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAI 450
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                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RDACLEIRLHMREMGIAAGVPIEPDSQTRLLDATMNMEGVLLAGVPGAGGFDAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHWDVYLRVIKS 368
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RDACLEIRLHMREMGIAAGVPIEPDSQTRLLDATMNMEGVLLAGVPGAGGFDAV 54
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74.18;
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                                                                     Score 204; DB 10;
Pred. No. 6.8e-11;
8; Mismatches 6;
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Pred. No. 6.8e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                    360
                                                                       216 LLIGWTGS-PASTSDLVDRV---HQSKEEKQAAYEQFLMKSRLCVETMINGFN-----
                                                                                                            300
                                                                                                                                                 162
                                                                                                                                                                                 241 FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT-EFSLPPLMN
                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                             183
                                                                                                                                                                                                                                                                                                                                    123 LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL 182
                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                                                                                                                                                            63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTIVKLTS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                  DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE 419
                                                                                                            LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW
                                                                                                                                                 GDIAASCYGG--WIAFSTFDHDWVNQKVT----TETLTDLLAMDWPELMIFPLKVPKQLR
                                                                                                                                                                                                                        GSSGAVTVGTVKALNIFYDLGL:
                                                                                                                                                                                                                                                         GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240
                                                                                                                                                                                                                                                                                                                                                                         ---RRNGELVLDIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                             IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT- 60
                                                                                                                                                                                                                                                                                                ----SFYHLK-----RKYGL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILING DATE: 2000-05-26
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TGKIS-VIQKQITKNRQ------LLAELSSLTGVVIE
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Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                         -ENPF----HYVLAAIHL-TEKYAQEQNKEL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 12866
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 108;
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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218 EVLIGWTGSPASS-PHFVSEVKRLK-SDP
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                                                                                                                                                                                                                                                                                                                   63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122
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APPLICATION NUMBER: 60/191,078
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                               NLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDH
                                                                                                                                          GLGSSAAVLVSVIKVLNEFYDM
                                                                                                                                                                          GLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG
                                                                                                                                                                                                               LNYVVTAIEIFEQYAKSCDIAMKHFHLTIDS-----NLDDSNG------HKY 118
                                                                                                     FDVSCAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLM
                                                                                                                                                                                                                                                                                                                                                      IQVKAPGKLYIAGEYAVTE-PGYKSVLIALDRF--VTATIEE-----TD----
                                                                    -DIAVSVYSGWLAYSTFDHEWVKH-QIEDT--
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o. US20020061569A1
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                                                                                                                                                                                                                                                                                 -QYKGTIHSKALHHNPVTFSRD---EDSI--VISDPHAAKQ-
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                                                                ----TVEEVLIKNWPGLHIEPLQAPENM
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LENGTH: 345
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166
                                245 CAVY-GSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE-FSLPPLMNLFL 302
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                                                                                                              185 SAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSGFDVS
                                                                                                                                                    79 VTAIEIFEQYAKSCDIAMKHFHLTIDS:
                                                                                                                                                                                                                                40 ---QYKGTIHSKALHHNPVTFSRD---EDSI--VISDPHAAKQ------LNYV 78
                                                                                                                                                                                                                                                                  67 RESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQGLDIT 126
                                                                                                                                                                                                                                                                                                                                            7 APGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTSPQLS 66
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VSVYSGWLAYSTFDHEWVKH-QIEDT
                                                                        SAAVLVSVIKVLNEFYDM-
                                                                                                                                                                                        ILGSNDFYSYRNQIESA--GLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGLGS 184
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Xu, H. Howard
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Trawick, John D.
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                                                                          -----KLSNL-YIYKLAVIANMKLQSLSSCG-DIA
                                                                                                                                                                                                                                                                                                                                                                                  57; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 133.5;
Pred. No. 0.
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-TVEEVLIKNWPGLHIEPLQAPENMEVLI
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US-09-909-745-26
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745
CURRENT FILING DATE: 2001-07-20
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TYPE: PRT
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VSHATIETVLRTTL--
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                             AASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAI 453
                                                                                                   KLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGE 412
                                                                                                                                                                     SLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLS 352
                                                                                                                                                                                                            -PSGIDNTVSAYGN---
                                                                                                                                                                                                                                             VGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVT----GLPLNEVIGTILKGKWDNKRTEF 292
                                                                                                                                                                                                                                                                              GSGLGSSASFCVALAAALLAYTDSVSL-DLKHQGWLSFGEKDLELVNKWAFEGEKIIHGK
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97; Conserv
                                                                                                                                      -----IMAFVFSAVDSISNELT
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21.0%;
--KYKLASKLTGAGGGGCVLTL
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                                                                  TPDE - - LSVTE - - KEEKIEELMEMNQGML
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Pred. No. 0.
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0.0084;
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344
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RESULT 12
US-09-925-388-8
; Sequence 8, Application US/09925388
; Publication No. US20030054523A1
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US-09-909-745-23
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                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: HOSHINO, Tatsuo
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: ISOPRENOID PRODUCTION
FILE REFERENCE: ISOPRENOID PRODUCTION
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APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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20.9%;
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Pred. No. 0.015;
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CURRENT APPLICATION NUMBER: US/09/925,388 CURRENT FILING DATE: 2001-08-09

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; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-925-388-8
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Query Match
                                                                                                 SEQ ID NO 4
LENGTH: 1477
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                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                              NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US97/04707
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/155,614
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 08/617,697
PRIOR FILING DATE: 1996-04-01
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/092,880 CURRENT FILING DATE: 2002-03-08
                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/306,595
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
                                                            ORGANISM: Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKD-KESLHKLLLQ 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 4.5%;
Local Similarity 21.6%;
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Pred. No. 0.091;
4; Mismatches 190
Score 108.5;
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Length 1477;
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                                                                                                                                                                                NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 534
TYPE: PRT
                                                                      Matches
                                                                                     Query Match
Best Local (
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                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/077,023 CURRENT FILING DATE: 2002-02-15 PRIOR APPLICATION NUMBER: 60/272,107 PRIOR FILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: 60/209,811 PRIOR FILING DATE: 2000-66-06
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: 240U, XIA-DI
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: IMMUNOMODULATION
FILE REFERENCE: 3053-4071US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MIKESELL, APPLICANT: CHANG, F
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                                183 GSSAAMTTAVVAALLHY-----LGVVDLSDPCKEGKFGC------SDLDVIHMI 225
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GSAYANRTALFPDLLAQGNASLRLQRVRVAD---EGSFTCFVSIRDFGSAAVSLQVAAPY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNAAESNGA-NSKPEVAKTG----LGSSAAMTTAVVAALL-----HYLGVVDLSDPCKE
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                                                                    Similarity
97; Conserv
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LU, PIN
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                                                                                     Score 101.5;
Pred. No. 1.9;
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B; Mismatches
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| | 324 252 | 283 GKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQM : : : : : | Db Qy |
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| | 282 192 | 26 AQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK :: | Db 04 |
| | 225 142 | 183 GSSAAMTTAVVAALLHYLGVVDLSDPCKEGKEGCSDLDVIHMI : : | B 8 |
| 23; | Gaps | Query Match 3.9%; Score 101.5; DB 10; Length 534; Best Local Similarity 22.8%; Pred. No. 1.9; Matches 97; Conservative 48; Mismatches 136; Indels 145; Ga | X # O |
| | | TYPE: PRI ORGANISM: Homo sapiens 09-875-338-7 | ; ; |
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| | • | sequence /, Application 05/098/5338 Patent No. US20020095024A1 GENERAL INFORMATION: | |
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| | | 469 VIVGLS 474 | 망 |
| | | TSG | Qy |
| | 494 468 | 447 FDAIFAITLGDSGTKLTQAWSSHNVLALLVREDPHGVCLESGDPRTTC | D 04 |
| | 419 | YSKPSMTLEPNKDLRPGDTVTTTCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGL | В |
| | 446 | 415SVPIEPESQTQLLDSTMSAEGVLLAGVPGAGG | Qy |
| | 359 | 300 GRDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAP | Db |
| | 414 | IKELLEAREAMLRIRILMRQMGEAA | Ş |
| | 299 | 253 EDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTE | 망 |
| | 383 | 325 SDPEKARENWONLSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHA-TE | Qγ |
| | 252 | 193 SQMANEQGLEDVHSILRVVLGANGTYSCLVRNPVLQQDAHSSVTITPQRSPTGAVEVQVP | 물 5 |
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| | 282 | 226 AQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILK | ₽ & |

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| 495 469 | 447 420 | 415 360 | 384 300 | 325 253 |
| 495 ITSGVS 500 : : 469 VTVGLS 474 | 447 FDAIFAITLGDSGTKLTQAWSSHNVLALLVREDPHGVCLESGDPRTTC 494 | 415SVPIEPESQTQLLDSTMSAEGVLLAGVPGAGG 446 | 384 PINEAIIKELLEAREAMLRIRILMRQMGEAA 414 :: | 325 SDPEKARENWQNLSDANLELETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHA-TE 383. |
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Search completed: April 26, 2003, 13:02:22 Job time: 22 secs

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Maximum DB seq length: 2000000000
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2581
1 MAVVASAPGKVLMTC
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/paa/US101_COMB.pep:
/cgn2_6/ptodata/1/paa/US102_COMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 7 TTC 7.TO | 61 3 611 37 176-60-301-300-36000 | 61.2 511 26 US-10-219-999-40847 | 503 24 US-10-036-959B-12 | 74.8 503 1 PCT-US02-24048A-12 | 23 US-09-988-863A-2 | No. Score Match Length DB ID D | Result Query | c |
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| equenc | 909 510 | uence 24, Ap | e 24, | 24, | 17922, | e 17922, | 7, | equence 13279, | equence 6401, | 7023, | equence 4975, A | 1496 | e 7023, A | e L | 14967, | 2162, | 177, 1 | e 8406, | 8406, | e 3406 | ce 3406 | ence 3406, | 3740 | 22, | Ø | e 22, | equence 3218, | e 6588 | 6223, | equence 42346, | e 55 | e 662 | e 8340 | e 6629 | 6 | 4 |

ALIGNMENTS

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| Db | Qy | Db | Qy | Matches 505; Conserv | Query Match | US-09-988-863A-2 | : TYP | ; LEN | ; SEQ ID NO 2 | ; SOFTWARE: PatentIn Ver. 2.1 | ; NUMBER OF SEQ ID NOS: 5 | ; CURRENT FILING DATE: 2001-11-21 | ; CURF | ; FILE REFERENCE: Le A 35 018 | ; TITLE OF INVENTION: Plant phosphomevalonate kinases | ; APPLICANT: Bayer AG | ; GENERAL INFORMATION: | ; Sequence 2, Application US/09988863A | US-09-988-863A-2 | RESULT 1 |
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PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 16
SOFTWARE: MICROSOFT Office 97
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application PC/TUS0224048A
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours & Company
TITLE OF INVENTION: Genes Involved in the Bic
TITLE OF INVENTION: brasiliensis Latex
FILE REFERENCE: CL1792 PCT
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74.1%; Pred. No. 5.96
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; SOFTWARE: Microsoft Office 9:
; SEQ ID NO 12
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Hevea brasiliensi:
US-10-036-959B-12
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Sequence 12, Application US/10036959B
Sequence 12, Application US/10036959B
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours & Company
APPLICANT: Hallahan, David L.
APPLICANT: Keiper-Hrynko, Natalie
TITLE OF INVENTION: Genes Involved in the Biosynthesis
TITLE OF INVENTION: brasiliensis Latex
FILE REFERENCE: CL-1792
CURRENT APPLICATION NUMBER: US/10/036,959B
CURRENT FILING DATE: 2002-05-10
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US-10-219-999-40847
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SEQ ID NO 40847
LENGTH: 511
TYPE: PRT
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Local Similarity 62.6%;
les 321; Conservative (
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Kovalic, David K.
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RESULT 6
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SEQ ID NO 16899
LENGTH: 511
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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Best Local Sim
Matches 321;
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TITLE OF INVENTION: CONA SEQUENCES AND USI
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
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                                                                                                                        KPEVAKTGLGSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCS--DLDVIHMIAQTSHC
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                                                             LPLLVREDCRGVSLEDADPRTREVSAAVSSIQI
                                                                                                                                                     EAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWSSHNV
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Kovalic, David K.
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Sequence 83408, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09

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; LOCATION: 1..499
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-83408
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APPLICANT: N. ALEXANDROV et al
                                                                 SEQ ID NO 83407
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                                                                                                                 TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                       TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
                                                                                   NUMBER OF SEQ ID NOS: 85364 SOFTWARE: PatentIn version
                                   TYPE: PRT
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OTHER INFORMATION: Xaa
         ORGANISM: Zea mays subsp. mays
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FEATURE:
                                                  ENGTH: 535
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PatentIn version 3.1
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NAME/KEY: misc_feature
: LOCATION: 1.535
: OTHER INFORMATION: Ceres
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 66289
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Best Local
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                                                                                                                                                                                                                                                                                                                               APPLICANT: N. ALEXANDROV et al
                                                                 NAME/KEY: misc_feature LOCATION: 1..535
OTHER INFORMATION: Xaa
                                                                                                                              TYPE: PRT
ORGANISM: Zea mays subsp.
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OTHER INFORMATION: Xaa
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LOCATION: 1..535
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Matches 277
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                                                                                                                                                                                                                                                                                 SEQ ID NO 66290
LENGTH: 326
                                                                                              Matches
                                                                                                                       Query Match
                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..326
OTHER INFORMATION: Xaa is a
NAME/KEY: misc_feature
LOCATION: 1..326
OTHER INFORMATION: Ceres Se
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                         ORGANISM: Zea mays subsp.
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           TSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDN 287
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                                     GEKCKPEVAKTGLGSSAAMTTSVVAALLHYLGVVSLSCPGQSSGDNTTRRELDLVHSIAQ
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Pred. No. 5.1e-87;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 83409
LENGTH: 326
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Best Local Similarity
Matches 198; Conserv
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LOCATION: 1.326
OTHER INFORMATION: Xaa i
NAME/KEY: misc_feature
LOCATION: 1.326
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CURRENT FILING DATE: 2000-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
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TYPE: PRT
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                                                                       RQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQAWS
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US-09-708-427-66291
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GENERAL INFORMATION:
                                                                                                                                                                                                                                    Sequence 55015, Application US/10219999 GENERAL INFORMATION:
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Best Local Similarity
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                                                                           APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
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CURRENT FILING DATE: 2000-11-09
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             PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
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 NUMBER OF SEQ ID NOS: 63520
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Kovalic, David K.
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                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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; TYPE: PRT
; ORGANISM: Zea mays
US-10-219-999-55015
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US-10-219-999-42346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stein, Joshua
TITLE OF INVENTION: CNA SEQUENCES AND USES
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/324,109 PRIOR FILING DATE: 2001-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 GTILKGKWDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWOMSDPEKARENWONL 337
                                                                                                                                                                                                                                                                     225 IAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGK 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 DLDVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVI 277
405 ILMRQMGEAASVPIEPESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSGTKLTQ 464
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                                                                                                                                                                                                                                         2 IAQSAHCLAQGKIGSGFDVSAAVYGSQRYVRFSPEILSSAQ-AIGGTVLPDVVSDVLTQR 60
                                                                                                                                                                  WDNKRTEFSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLEL 344
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                                                                                        ETKLNDLSKLAKDHWDVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIR 404
                                                                                                                                           WDHENKQFSLPPLWTLLLGEPGTGGSSTPSMVGSVKRWLKSDPEKSRDTWSKLAIANSTL 120
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                                                ENQLRILKGLSENHHEAYESMVRSCSRLTYGKWAEVATNQHQELIIRSLLAARDACLEIR
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                                                                                                                                                                                                                                                                                                                                                                     32.5%; Score 839.5; DB: 59.3%; Pred. No. 7.5e-74
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US-09-708-427-65887
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US-60-312-544-6223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CUMA SEQUENCES AND USES FOR PLANT IMPROVEMENT FILE REFERENCE: 38-.0(52726)A CURRENT APPLICATION NUMBER: US/60/312,544 CURRENT FILING DATE: 2001-08-15 NUMBER OF SEQ ID NOS: 10730 SEQ ID NO 6223 LENGTH: 281
                                                                                                                                                                                                   Sequence 65887, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65887
LENGTH: 359
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                                                                                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, Jingdong APPLICANT: Stein, Joshua
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ORGANISM: Zea mays subsp. mays
                      TYPE: PRT
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Kovalic, David K.
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Pred. No. 7.5
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hes 70;
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; NAME/KEY: misc_feature
; COCATION: 1..359
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..359
; OTHER INFORMATION: Ceres Seq. ID 1929648
US-09-708-427-65887
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Best Local Similarity
Matches 153; Conserv
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293 DLVHTIAQSAHCLAQGKIGSGFDVSAAVYGSQRYVRFSPEILSSAQ-AIGG 342
                                                                                                                                                                                      49 ESWAWKWTDVKLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLAT 108
                DVIHMIAQTSHCLAQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTG
                                                        Conservative
                                                                                                                                                                                                                             28.0%; Score 722.5; DB 66.2%; Pred. No. 5e-62; tive 26; Mismatches
                                                                                                                                                                                                                                                           DB 21;
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Search completed: April 26, 2003, 13:00:27 Job time: 151 secs

OMEN WARE SHAM CHANGE

Copyright

GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.

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Title:
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              Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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                                                DTDTCQNKAT-ISVRAGQFPSDASTWVYCISKPSASASASAGEDGEDGEEGGDGTLYLKL 126
                                                                                 KPESWAWKWTDVKLTSPQLSRES---MYKLSLNHLTLQSVSASD-----
                                                                                                                VVSSPGKVLIAGGYLVLDTHYSGLVIGTSSRFYSCVSSRATSSRATSSTPSIDADTNNDI
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Pred. No. 5.
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SCOTTWARE: Microsoft Office 9:
SEQ ID NO 2
LENGTH: 179
TYPE: PRT
ORGANISM: Oryza sativa
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                                                Sequence 3740, Application US/10369493 GENERAL INFORMATION:
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gre-
APPLICANT: Slater, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-11-05
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, Gregory J.
, Steven C.
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Pred. No. 2.5e-44;
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Length 423;

Indels 100;

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GENERAL INFORMATION:

APPLICANT: CAO, YONGWEI

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

FITTLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21
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US-10-369-493-3740
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION UNLERS: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3740
                                                                                                                                                                                                                                                                    Sequence 2162,
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                    Application US/10369493
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                       ORGANISM: Aspergillus fumigatus US-09-675-784A-13279
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SEQ ID NO 2162
                                                                                                    NUMBER OF SEQ
SEQ ID NO 13279
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                                                                                                                                                                                                                         TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC TITLE OF INVENTION: AND USES THEREFOR FILE REFERENCE: 2976-4020US1
                                                                                                                                        PRIOR APPLICATION NUMBER: 60/156,338 PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/675,784A CURRENT FILING DATE: 2000-09-29
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NOLLING, JORK
ZENG, QIANDONG
GREENE, JONATHAN R.
                                                                                                                                                                                                                                                                                                                                                                      SHAW, KAREN J.
SHIMER JR., GEORGE
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Pred. No. 1.8e-35;
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US-09-909-745A-24
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                                                                                                                                                             SOFTWARE: Microsoft
SEQ ID NO 24
LENGTH: 451
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Best Local Similarity
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/433,242
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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30.1%;
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                                             Score 453.5;
Pred. No. 1.5e
72; Mismatches
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-EVKPESWAWK---
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1909
LENGTH: 451
TYPE: PRT
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                            112 KESLHKLLLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGA 171
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 102 KPNMDDYCNRNLFVIDIFSDD--AYHSQEDS---
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                                                                                 TDVKLTSPQLSRESMYKLSLNHLTLQS----VSASDSRNPFVEHAIQYAIAAAHLATEKD 111
                                                                                                                             TKLTQAWSSH -- NVLALLVREDPHGVCLESGDPRT 492
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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                                                                                                                                                                                         Score 453.5; DB (
Pred. No. 1.5e-32;
2; Mismatches 185
 -VTEHRG-
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 NKRLSFHS 144
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US-09-909-745A-16 ; Sequence 16, Application US/09909745A
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US-09-909-745A-20
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Best Local Similarity
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            CURRENT APPLICATION NUMBER: US/09/909,745A CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 09/433,242
                                                                      APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
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PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
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TITLE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
                                                                                                                       APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omola
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PRIOR FILING DATE: 1999-11-04
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Pred. No. 2.8e-12
12; Mismatches 1:
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Best Local Similarity
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US-10-282-122A-56929
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US-09-909-745A-18
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SEQ ID NO 18
LENCTH: 54
TYPE: PRT
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                                                                                                                                                                                                  APPLICANT:
APPLICANT:
          FILE REFERENCE: ELITRA.034A
CUURERNT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/909,745A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/433,242
PRIOR FILING DATE: 1999-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Famodu, Omolayo O. TITLE OF INVENTION: Squalene Synthesis Enzymes FILE REFERENCE: BB1112 US CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/107,241 PRIOR FILING DATE: 1998-11-05
                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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APPLICATION NUMBER:
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Haselbeck, Robert
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RESULT 13
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US-10-282-122A-56929
                                                                                                                      Sequence 5356, Application US/09134000C GENERAL INFORMATION:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13
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SOFTWARE: PatentIn version 3.1
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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FILING DATE: 2000-09-06
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APPLICATION NUMBER: 60/
FILING DATE: 2000-05-26
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Pred. No. 1.6e-07;
58; Mismatches 179;
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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5356
LENGTH: 370
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62
                                                                                                                                                                                                                                     FDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRT-EFSLPPLMN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                      PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG
TEALKNLCDLAESYTGA--AKSSGAGGGDCGIVIFRQKSGILPLMTAWEK:GITPL
                              PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVLAL
                                                                                                 DVYLRVIKSCSVLTSEKWVLHATEPINEAIIKELLEAREAMLRIRILMRQMGEAASVPIE
                                                                                                                                                                  LFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDLSKLAKDHW 359
                                                                                                                                                                                                                                                                                                         GSSAAMTTAVVAAL--LHYLGVVDLSDPCKEGKFGCSDLDVIHMIAQTSHCLAQGKVGSG 240
                                                                                                                                                                                                                                                                                                                                                                            LDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEVAKTGL 182
                                                                                                                                                                                                                                                                                                                                                                                                               ---RRNGELVLDIR-----ENPF----HYVLAAIHL-TEKYAQEQNKEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT-
                                                                                                                                   LLIGWTGS-PASTSDLVDRV---HQSKEEKQAAYEQFLMKSRLCVETMINGFN-----
                                                                                                                                                                                                    GDIAASCYGG--WIAFS----TFDHDWVNQKVATETLTDLLAMDWPELMIFPLKVPKQLR
                                                                                                                                                                                                                                                                         GSSGAVTVGTVKALNIFYDLGL - - -
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106; Conserv
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                                                                 TGKIS-VIQKQITKNRQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 177.5; DB 5;
Pred. No. 1.7e-07;
8; Mismatches 179;
                                                                                                                                                                                                                                                                         -- ENEEIFKLSALAHLAVQGN-GSC
                                                                  -----LLAELSSLTGVVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 133;
350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                   419
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                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                        217
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                                                                    296
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                                                                                                                                     ; ORGANISM: Enterococcus US-09-134-000C-5356
                                                                                                                                                                                               SEQ ID NO 5356
LENGTH: 370
                                                                            Query Match
Best Local Similarity
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                      SOFTWARE: PatentIn
                                                                                                                                                                          TYPE: PRT
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VVASAPGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDVKLTS 62 : | | | : | | : | : | : | : | : | : |
                                                           106;
                                                           Conservative
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                                                                            6.9%;
                                                                                                                                                          faecalis
                                                           58;
                                                                         Score 177.5; DB 5
Pred. No. 1.7e-07;
                                                         Mismatches 179;
                                                                                              DB 5;
                                                           Indels 133;
                                                                                            Length
                                                           Gaps
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RESULT 14 US-09-134-000C-5356

Sequence 5356, Application US/09134000C GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al

| · | 292 FSLPPLMNLFLGEPGSGGSSTPSMVGAVKKWQMSDPEKARENWQNLSDANLELETKLNDL | VQ |
|-----|--|-------|
| | y 233 AQGKVGSGFDVSCAVYGSQRYVRFSPEVLSFAQVAVTGLPLNEVIGTILKGKWDNKRTE- 291 ; | g Q |
| | b 111 YQGKKIGLGSSGAVTIAVIRGLSLLYDLHLKDIDIFKLAAIAHIQ 155 | 밁 |
| | 178AKTGLGSSAAMTTAVVAA | Qy |
| | y 119 LLQGLDITILGSNDFYSYRNQIESAGLPLTPESLGTLAPFASITFNAAESNGANSKPEV- 177 | B 5 |
| | 66GIFSFKDWSHPFHLVB | 망 |
| • | Y 59 KLTSPQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKL 118 | Qy |
| | : : : :: : : : : : : | 망 |
| | 8 PGKVLMTGGYLVLEKPNAGLVLSTNARFYAIVKPINEEVKPESWAWKWTDV 58 | ρ |
| 3 ° | | |
| | ORGANISM: Alloiococcus otitidis CT-US02-36122-42 | P |
| | SEO ID NO 42 LENGTH: 362 TYPE: PRT | |
| | NUMBER OF SEQ ID NOS: 106 SOFTWARE: PatentIn version | ٠. ٠. |
| | | |
| | APPLICANT: Murphy, Ellen and Projan, Stephen, j. TITLE OF INVENTION: Allolococcus offitidis Infectious Disease Targets FILE REFERENCE: Application 1 | |
| | CT-US02-36122-42 Sequence 42, Application PC/TUS0236122 GEMERAL INFORMATION: | PC |
| | SULT 15 | RE |
| | b 297 TEALKNLCDLAESYTGAAKSSGAGGGDCGIVIFRQKSGILPLMTAWEKDGITPL 350 | рь |
| | y 420 PESQTQLLDSTMSAEGVLLAGVPGAGGFDAIFAITLGDSG-TKLTQAWSSHNVLAL 474 | Qy |
| | 267 | 망 |
| • | 360 DVYLRVIKSCSVLTSEKWVLHA | Qy |
| | 218 | 뮰 |
| | 300 LFLGEPGSGGSSTPSMVGAVK | Qγ |
| | b 164 GDIAASCYGGWIAFSTFDHDWVNQKVATETLTDLLAMDWPELMIFPLKVFKQLR 217 | Db |
| | 241 FDVSCAVYGSQRYVRFSPEVI | VΩ |
| | | 망 |
| | 183 GSSAAMTTAVVAALLHYLGVVDLSDPCKEGKFGCSDLDVTHMTAOTSHCLAOGKVGSG 24 | Q |
| | b 99SPYHLKVTSELDSSNGRXYGL 119 | B 5 |
| | יייייייייייייייייייייייייייייייייייייי | 2 |
| | Y 63 PQLSRESMYKLSLNHLTLQSVSASDSRNPFVEHAIQYAIAAAHLATEKDKESLHKLLLQG 122 b 63RRNGELVLDIR | P Q |
| | 4 IEVTTPGKLFIAGEYAVVEPGHPAIIVAVDQFVTVTVEETTDEGSIQSAQYSSLPIRWT- 62 | 뫄 |

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Qy
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В
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: | | : : | | : 347 ILPLRLDIVENGACYD 362
      471 VLALLVREDPHGVCLE 486
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Search completed: April 26, 2003, 13:01:55 Job time : 84 secs

THE PACE BLANK (18970)